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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:41 ; Search time 22 Seconds  
(without alignments)  
64.100 Million cell updates/sec

Title: SEQ1

Perfect score: 183

Sequence: 1 mcsnlstcvlgklsqelhkltqyprntgsgtpg 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	178	97.3	136	1	CALL_ONCKE
2	159	86.9	32	1	CAL_ANGJA
3	157	85.8	32	1	CAL2_ONCKE
4	157	85.8	138	1	CAL_CHICK
5	154	84.2	32	1	CAL3_ONCKI
6	108	59.0	136	1	CAL0_RAT
7	101	55.2	141	1	CAL0_HUMAN
8	100	54.6	136	1	CAL0_MOUSE
9	90	49.2	92	1	CAL_CANFA
10	72	39.3	143	1	CAL_SHEEP
11	68	37.2	402	1	KPPR_SPIOL
12	67	36.6	397	1	KPPR_MESCR
13	62	33.9	32	1	CAL_BOVIN
14	61	33.3	32	1	CAL_PIG
15	61	33.3	395	1	KPPR_ARATH
16	61	33.3	404	1	KPPR_WHEAT
17	54.5	29.8	213	1	NO2B_SOYBN
18	54.5	29.8	401	1	SP2B_BACSU
19	52	28.4	375	1	KPPR_CHLRE
20	51	27.9	491	1	AZAP_MOUSE
21	49	26.8	400	1	EX7L_CLOPE
22	49	26.8	529	1	Y98H_HUMAN
23	49	26.8	939	1	EAE_ECO27
24	49	26.8	3038	1	TRIO_HUMAN
25	48	26.2	180	1	REL5_SCHPO
26	48	26.2	224	1	NUOB_BUCAL
27	48	26.2	425	1	NG79_SCHPO
28	48	26.2	747	1	YME1_YEAST
29	48	26.2	1058	1	S185_YEAST
30	47.5	26.0	1868	1	YHD0_YEAST
31	47	25.7	240	1	IPT_AGRY4
32	47	25.7	282	1	YODC_ECOLI
33	47	25.7	391	1	Z072_XENLA

34 47 25.7 474 1 MEC3\_YEAST  
35 47 25.7 661 1 CA01\_MOUSE  
36 47 25.7 661 1 CA01\_RAT  
37 47 25.7 671 1 HPS4\_MOUSE  
38 47 25.7 1491 1 AT7A\_MOUSE  
39 47 25.7 1492 1 AT7A\_RAT  
40 46.5 25.4 1916 1 RIF1\_YEAST  
41 46 25.1 245 1 Y542\_CHLPN  
42 46 25.1 262 1 APAL\_BRARE  
43 46 25.1 332 1 KPPR\_SYNY3  
44 46 25.1 371 1 KLOM\_EISFO  
45 46 25.1 385 1 YDEM\_ECOLI

Q02574 saccharomyc  
Q910h0 mus musculus  
P07872 rattus norv  
Q99kg7 mus musculus  
Q64430 mus musculus  
P70705 rattus norv  
P29539 saccharomyc  
Q92810 chlamydia p  
O42363 brachydanio  
P37101 synchocyst  
O15991 eisenia foe  
P76134 escherichia

## ALIGNMENTS

RESULT 1  
CALL\_ONCKE STANDARD; PRT; 136 AA.  
AC P01263;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Calcitonin 1 precursor.  
OS Oncorhynchus keta (Chum salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8018;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88083644; PubMed=3691820;  
RA Poeschl E., Lindley I., Hofer E., Seifert J.M., Brunowsky W.,  
Besemer J.;  
RT "The structure of procalcitonin of the salmon as deduced from its  
RT cDNA sequence.";  
RL FEBS Lett. 226:96-100(1987).  
RN [2]  
RP SEQUENCE OF 85-116.  
RX MEDLINE=70053602; PubMed=5261048;  
RA Niall H.D., Keutmann H.T., Copp D.H., Potts J.T. Jr.;  
RT "Amino acid sequence of salmon ultimobranchial calcitonin.";  
Proc. Natl. Acad. Sci. U.S.A. 64:771-778(1969).  
RN [3]  
RP SYNTHESIS OF CALCITONIN.  
RX MEDLINE=70067983; PubMed=5361911;  
RA Guttman S., Pless J., Huguenin R.L., Sandrin E., Bossert H.,  
Zehnder K.;  
RT "Synthesis of salmon calcitonin, a high activity hypocalcemic  
RT hormone.";  
RL Helv. Chim. Acta 52:1789-1795(1969).  
RN [4]  
RP STRUCTURE BY NMR OF CALCITONIN.  
RX MEDLINE=91120767; PubMed=1991104;  
RA Meadows R.P., Nikonowicz E.P., Jones C.R., Bastian J.W.,  
Gorenstein D.G.;  
RT "Two-dimensional NMR and structure determination of salmon calcitonin  
RT in methanol.";  
RL Biochemistry 30:1247-1254(1991).  
RN [5]  
RP STRUCTURE BY NMR OF CALCITONIN.  
RX MEDLINE=91255658; PubMed=2043752;  
RA Meyer J.-P., Pelton J.T., Hoflack J., Saudek V.;  
RT "Solution structure of salmon calcitonin.";  
RL Biopolymers 31:233-241(1991).  
RN [6]  
RP STRUCTURE BY NMR OF CALCITONIN.  
RX MEDLINE=92031485; PubMed=1931969;  
RA Motta A., Pastore A., Goud N.A., Castiglione Morelli M.A.;  
RT "Solution conformation of salmon calcitonin in sodium dodecyl sulfate  
RT micelles as determined by two-dimensional NMR and distance geometry  
RT calculations.";

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RL Biochemistry 30:10444-10450(1991).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- PHARMACEUTICAL: Available under the names Calcimar (Rhône-Poulenc
CC Rorer), Miacalcin (Novartis) or Forcalcitonin (Unigene). Used for
CC the treatment of Paget's disease and hypercalcemia in malignancy.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----
DR EMBL: Y00765; CAA68734.1; ..
DR PIR: A01530; TCON
DR PIR: A31229; A31229.
DR HSSP: P01262; LBKU.
DR InterPro: IPR001693; Calcitonin-like.
DR InterPro: IPR001935; Calcitonin_A.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00270; CALCITONIN.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
DR Cleavage on pair of basic residues; Amidation; Hormone; Signal;
KW Pharmaceutical.
FT SIGNAL 1 25
FT PEPTIDE 83 114 CALCITONIN 1.
FT DISULFID 83 89
FT MOD_RES 114 114
FT SEQUENCE 136 AA; 15179 MW; BDD867AE113B2A8 CRC64;

Query Match 97.3%; Score 178; DB 1; Length 136;
Best Local Similarity 100.08; Pred. No. 1.1e-18; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
DB 83 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 115

RESULT 2
CAL_ANGJA
ID CAL_ANGJA STANDARD; PRT; 32 AA.
AC P01262;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcitonin.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE.
RA Noda T., Narita K.;
RT "Amino acid sequence of eel calcitonin.";
RL J. Biochem. 79:353-359(1976).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=99315214; PubMed=10387083;
RA Hashimoto Y., Tama K., Nishikido J., Yamamoto K., Inazu T.,
RA Valentine K.G., Opella S.J.;
RT "Effects of glycosylation on the structure and dynamics of eel
RT calcitonin in micelles and lipid bilayers determined by nuclear
RT magnetic resonance spectroscopy.";
RL Biochemistry 38:8377-8384(1999).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION

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CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC PIR: A01529; TCEP.
CC PDB: 1BKU; 18-MAR-99.
CC InterPro: IPR001693; Calcitonin-like.
CC InterPro: IPR001935; Calcitonin_A.
CC Pfam: PF00214; Calc_CGRP_IAPP; 1.
CC PRINTS: PR00270; CALCITONIN.
CC SMART: SM00113; CALCITONIN; 1.
CC PROSITE: PS00258; CALCITONIN; 1.
CC Hormone; Amidation; 3D-structure.
KW DISULFID 1 7
FT MOD_RES 32 32
FT SEQUENCE 32 AA; 3418 MW; AFC93549F8048922 CRC64;

Query Match 86.9%; Score 159; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 1.3e-16; Indels 0; Gaps 0;
Matches 29; Conservative 2; Mismatches 1;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
DB 1 CSNLSTCVLGKLSQELHKLQTYPRTDVGAGTP 32

RESULT 3
CAL2_ONCKE
ID CAL2_ONCKE STANDARD; PRT; 32 AA.
AC P01264;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calcitonin 2.
OS Oncorhynchus keta (Chum salmon), and
OS Oncorhynchus nerka (Sockeye salmon).
OS Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 8023, 8017;
RN [1]
RP PRELIMINARY SEQUENCE.
RA Keutmann H.T., Lequin R.M., Habener J.F., Singer F.R., Niall H.D.,
RA Potts J.T. Jr.;
RT "Chemistry and physiology of the calcitonins: some recent advances.";
RL (In) Taylor S. (eds.);
RL Endocrinology 1971: proceedings of the third international symposium,
RL pp.316-323, Heinemann Medical Books, London (1972).
RN [2]
RP SYNTHESIS.
RX MEDLINE=73047885; PubMed=4508400;
RA Pless J., Bauer W., Bossert H., Zehnder K., Guttman S.;
RT "Synthesis of two natural salmon calcitonins.";
RL Nature New Biol. 240:62-63(1972).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC PIR: C01531; TCON2C.
CC PIR: A01531; TCON2.
CC PIR: D01531; TCON2P.
CC HSSP: P01262; LBKU.
CC InterPro: IPR001693; Calcitonin-like.
CC InterPro: IPR001935; Calcitonin_A.
CC Pfam: PF00214; Calc_CGRP_IAPP; 1.
CC PRINTS: PR00270; CALCITONIN.
CC SMART: SM00113; CALCITONIN; 1.
CC PROSITE: PS00258; CALCITONIN; 1.
KW Hormone; Amidation.
FT DISULFID 1 7
FT MOD_RES 32 32
FT SEQUENCE 32 AA; 3387 MW; AFCB969AF807E7C2 CRC64;

Query Match 85.8%; Score 157; DB 1; Length 32;

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DR HSP: P01262; 1BKU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONINA.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Amidation; Alternative splicing;
KW Hormone; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT FT PROPEP 26 79
FT PEPTIDE 82 113 CALCITONIN.
FT PROPEP 118 138
FT DISULFID 82 88
FT MOD_RES 113 113
FT CONFLICT 56 56
FT SEQUENCE 138 AA; 1530 MW; 730B618CF724F248 CRC64;

Query Match 85.8%; Score 157; DB 1; Length 138;
Best Local Similarity 84.8%; Pred. No. 1.2e-15;
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps

QY 2 CSNLSTCVLGLSQELHKLQTYPTNTGSGTPG 34
D 1:|||||
DB 82 CASLSTCVLGLSQELHKLQTYPTDVGAGTPG 114
1:|||||

RESULT 5
CAL3_ONCKI STANDARD; PRT; 32 AA.
AC CAL3_ONCK1
ID P01265;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calcitonin 3.
OS Oncorhynchus kisutch (Coho salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8019;
RX [1]
RX PRELIMINARY SEQUENCE.
RA Reutemann H.T., Lequin R.M., Habener J.F., Singer F.R., Niall H.D.,
RA Potts J.T. Jr.;
RA "Chemistry and physiology of the calcitonins: some recent advances."
RL (in) Taylor S. (eds.);
RL Endocrinology 1971; proceedings of the third international symposium
RL pp.316-323, Heinemann Medical Books, London (1972).
RX [2]
RX SYNTHESIS.
RX MEDLINE=73047885; PubMed=4508400;
RA Pless J., Bauer W., Bossert H., Zehnder K., Guttman S.;
RA "Synthesis of two natural salmon calcitonins.";
RA Nature New Biol. 240:62-63(1972).
CC 1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC 1- MISCELLANEOUS: CALCITONIN 1 IS LESS ACTIVE THAN CALCITONINS 1 OR
CC 2. ONLY THIS SPECIES OF SALMON POSSESSES CALCITONIN 3.
CC 1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
DR HSP; P01262; 1BKU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONINA.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Hormone; Amidation.
FT DISULFID 1 7
FT MOD_RES 32 32
FT SEQUENCE 32 AA; 3419 MW; B57A3D9AF807E7C2 CRC64;

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Query Match 84.2%; Score 154; DB 1; Length 32;  
 Best Local Similarity 84.4%; Pred. No. 6.7e-16;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSCTVGLKLSQELHKLQTYPTNTGSGTP 33  
 DQ 1 CSNLSCTVGLKLSQELHKLQTYPTNTGAGVP 32

RESULT 6  
 ID CALO\_RAT STANDARD; PRT; 136 AA.  
 AC P01257;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Calcitonin precursor.  
 GN CALCA OR CALC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81225842; PubMed=6264603;  
 RA Jacobs J.W., Goodman R.H., Chin W.W., Dee P.C., Habener J.F.,  
 RA Bell N.H., Potts J.T. Jr.  
 RT "Calcitonin messenger RNA encodes multiple polypeptides in a single  
 precursor."  
 RL Science 213:457-459(1981).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87025913; PubMed=6400492;  
 RA Rosenfeld M.G., Amara S.G., Evans R.M.;  
 RT "Alternative RNA processing events as a critical developmental  
 regulatory strategy in neuroendocrine gene expression."  
 RL Biochem. Soc. Symp. 49:27-44(1984).  
 RN [3]  
 RP SEQUENCE OF 83-136 FROM N.A.  
 RX MEDLINE=81034790; PubMed=6933496;  
 RA Amara S.G., David D.N., Rosenfeld M.G., Roos B.A., Evans R.M.;  
 RT "Characterization of rat calcitonin mRNA."  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4444-4448(1980).  
 RN [4]  
 RP SEQUENCE OF 85-116.  
 RX MEDLINE=76210265; PubMed=12781175;  
 RA Raulais D., Hagaman J., Ontjes D.A., Lundblad R.L., Kingdon H.S.;  
 RT "The complete amino-acid sequence of rat thyrocalcitonin."  
 RL Eur. J. Biochem. 64:607-611(1976).  
 CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF  
 CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION  
 CC OF THOSE IONS IN THE BONES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: THE CALCITONIN PRECURSOR AND THE CALCITONIN  
 CC RELATED PEPTIDE PRECURSOR ARE OBTAINED BY TISSUE-SPECIFIC SPLICING  
 CC OF THE SAME GENE.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; V01230; CAA24540.1;  
 CC EMBL; V01228; CAA24538.1;  
 CC EMBL; V01223; CAA24539.1;  
 CC EMBL; M26137; AAA40849.1;  
 CC EMBL; M31027; AAB59681.1;  
 CC EMBL; L00109; AAB59681.1; JOINED.  
 CC EMBL; L00110; AAB59681.1; JOINED.

DR PIR; A01525; TCRT.  
 DR HSP; P01262; IBRU.  
 DR InterPro; IPR001693; Calcitonin-like.  
 DR InterPro; IPR001935; Calcitonin\_A.  
 DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.  
 DR PRINTS; PRO0270; CALCITONIN.  
 DR SMART; SM00113; CALCITONIN; 1.  
 DR PROSITE; PS00258; CALCITONIN; 1.  
 KW Cleavage on pair of basic residues; Signal; Amidation; Hormone;  
 KW Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 25  
 FT PROPEP 26 82  
 FT PEPTIDE 85 116  
 FT PROPEP 121 136  
 FT DISULFID 85 91  
 FT CARBOHYD 87 87  
 FT MOD\_RES 116 116  
 SQ SEQUENCE 136 AA; 15103 MW; A197358A802222F7 CRC64;  
 Query Match 59.0%; Score 108; DB 1; Length 136;  
 Best Local Similarity 54.5%; Pred. No. 1.4e-08;  
 Matches 18; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 CSNLSCTVGLKLSQELHKLQTYPTNTGSGTPG 34  
 DQ 85 CGNLSCTMLGTYTDLNKFHTFPQTSGVGAPG 117

RESULT 7  
 ID CALO\_HUMAN STANDARD; PRT; 141 AA.  
 AC P01258; Q13937;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Calcitonin precursor [Contains: Calcitonin; Katacalcin (Calcitonin  
 DE carboxyl-terminal peptide) (CCP) (PDN-21)].  
 GN CALCA OR CALCI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=89386053; PubMed=25711128;  
 RA Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;  
 RT "Structure and methylation of the human calcitonin/alpha-CGRP gene."  
 RL Nucleic Acids Res. 17:6999-7011(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=84132556; PubMed=6546550;  
 RA le Moulec J.M., Jullienne A., Chenais J., Lasmoles F.,  
 RA Gullana J.M., Milhaud G., Moukhtar M.S.;  
 RT "The complete sequence of human preprocalcitonin."  
 RL FEBS Lett. 167:93-97(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=85166259; PubMed=3872459;  
 RA Jonas V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,  
 RA Mermod J.-J., Evans R.M., Rosenfeld M.G.;  
 RT "Alternative RNA processing events in human calcitonin/calcitonin  
 RT gene-related peptide gene expression."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=86164952; PubMed=3485540;  
 RA Riley J.H., Edbrooke M.R., Craig R.K.;  
 RT "Ectopic synthesis of high-Mr calcitonin by the BEN lung carcinoma  
 RT cell line reflects aberrant proteolytic processing."  
 RL FEBS Lett. 198:71-79(1986).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=87213363; PubMed=3034287;

RA Craig R.K., Riley J.H., Edbrooke M.R., Broad P.M., Poord S.M.,  
RA Al-Kazwini S.J., Holman J.J., Marshall I.,  
RT "Expression and function of the human calcitonin/alpha-CGRP gene in  
RL health and disease."  
RL Biochem. Soc. Symp. 52:91-105(1986).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Thyroid carcinoma;  
RX MEDLINE=92105127; PubMed=1761559;  
RA Minvielle S., Giscard-Dartevelle S., Cohen R., Taboulet J., Iabrye F.,  
RA Julienne A., Rivaille P., Milhaud G., Moukhtar M.S., Lasmoles F.,  
RT "A novel calcitonin carboxyl-terminal peptide produced in medullary  
RT thyroid carcinoma by alternative RNA processing of the  
RL calcitonin/calcitonin gene-related peptide gene."  
RL J. Biol. Chem. 266:24627-24631(1991).  
RN [7]  
RP SEQUENCE OF 49-141 FROM N.A. (ISOFORM 1).  
RX MEDLINE=85230541; PubMed=2408883;  
RA Edbrooke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D.,  
RA Pettengill O.S., Craig R.K.,  
RT "Expression of the human calcitonin/CGRP gene in lung and thyroid  
RT carcinoma."  
RL EMBO J. 4:715-724(1985).  
RN [8]  
RP SEQUENCE OF 48-83 FROM N.A.  
RX MEDLINE=85022523; PubMed=6148938;  
RA Nelkin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.,  
RA Baylin S.B.,  
RT "Structure and expression of a gene encoding human calcitonin and  
RT calcitonin gene related peptide."  
RL Biochem. Biophys. Res. Commun. 123:648-655(1984).  
RN [9]  
RP SEQUENCE OF 85-116.  
RX MEDLINE=72162720; PubMed=5760861;  
RA Neher R., Riniker B., Rittel W., Zuber H.,  
RA "Human calcitonin. Structure of calcitonin M and D."  
RL Helv. Chim. Acta 51:1900-1905(1968).  
RN [10]  
RP STRUCTURE BY NMR OF CALCITONIN.  
RX MEDLINE=91159414; PubMed=2001366;  
RA Motta A., Temussi P.A., Wunsch E., Bovermann G.,  
RT "A 1H NMR study of human calcitonin in solution."  
RL Biochemistry 30:2364-2371(1991).  
RN [11]  
RP CHARACTERIZATION OF KATACALCIN.  
RX MEDLINE=83166029; PubMed=6132180;  
RA Hillyard C.J., Myers C., Abeyasekera G., Steverson J.C.,  
RA Craig R.K., MacIntyre I.,  
RT "Katacalcine: a new plasma calcium-lowering hormone."  
RL Lancet 1:846-848(1983).  
CC -!- FUNCTION: CALCITONIN CAUSES A RAPID BUT SHORT-LIVED DROP IN THE  
CC LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE  
CC INCORPORATION OF THOSE IONS IN THE BONES.  
CC -!- FUNCTION: Katacalcine is a potent plasma calcium-lowering peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3 (AC  
CC P06881); ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; X15943; CAA34070.1; ALT\_SEQ.  
DR EMBL; X00356; CAA25103.1;  
DR EMBL; K03513; AAA52124.1;  
DR EMBL; M12666; AAA51913.1;  
DR EMBL; M12664; AAA51913.1; JOINED.  
DR EMBL; M12665; AAA51913.1; JOINED.

DR EMBL; X03662; CAA27299.1;  
DR EMBL; M64486; AAA58403.1;  
DR EMBL; M26095; AAA35501.1;  
DR PIR; A22716; TCHU.  
DR PIR; C22949; C22949.  
DR PIR; S07238; S07238.  
DR PIR; S07242; S07242.  
DR PIR; S07643; S07643.  
DR HSSP; P01262; 1BKU.  
DR Genew; HGNC:1437; CALCA.  
DR MIM; 114130;  
DR InterPro; IPR001693; Calcitonin-like.  
DR InterPro; IPR001935; Calcitonin A.  
DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.  
DR PRINTS; PR00270; CALCITONINA.  
DR SMART; SM00113; CALCITONIN; 1.  
DR PROSITE; PS00258; CALCITONIN; 1.  
KW Cleavage on pair of basic residues; Amidation; Alternative splicing;  
KW Hormone; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT PROPEP 26 82  
FT PEPTIDE 85 116 CALCITONIN.  
FT PEPTIDE 121 141 KATACALCIN.  
FT DISULFID 85 91  
FT MOD\_RES 116 116  
FT VARSPIC 134 141  
FT CONFLICT 92 92  
SQ SEQUENCE 141 AA; 15467 MW; 99622305DD8B286F CRC64;  
Query Match 55.2%; Score 101; DB 1; Length 141;  
Best Local Similarity 51.5%; Pred. No. 1.5e-07;  
Matches 17; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
QY 2 CSNLSTCVLKLQSLQELHKLQTYPRNTGSGTPG 34  
DB 85 CGNLSTCMLGTYTQDFNKFHTFPQTATGVGAPG 117  
-----  
RESULT 8  
CALO\_MOUSE  
ID CALO\_MOUSE STANDARD; PRT; 136 AA.  
AC P70160;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Calcitonin precursor.  
GN CALCA OR CALC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thyroid;  
RX MEDLINE=96400274; PubMed=8806650;  
RA Rehli M., Luger K., Beier W., Falk W.,  
RT "Molecular cloning and expression of mouse procalcitonin."  
RL Biochem. Biophys. Res. Commun. 226:420-425(1996).  
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF  
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION  
CC OF THOSE IONS IN THE BONES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2 (AC  
CC Q95JAO); are produced by alternative splicing.  
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
CC -----  
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CC -----

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CC -----
DR EMBL; X97991; CAA66630.1;
DR HSP; P01262; 1BKU.
DR MGD; MG1:2151253; Calca.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Signal; Amidation; Hormone;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 82
FT PEPTIDE 85 116 CALCITONIN.
FT PROPEP 121 136
FT DISULFID 85 91 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (PROBABLE).
FT MOD_RES 116 116 AMIDATION (G-117 PROVIDE AMIDE GROUP).
SQ SEQUENCE 136 AA; 15141 MW; B7F1DD27F7E10DE5 CRC64;

Query Match 54.6%; Score 100; DB 1; Length 136;
Best Local Similarity 51.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
   I I I I I I I I I I I I I I I I I I
DB 85 CGNLSTCVLGTYTQDLNKPFTFPQTSIGVEAPG 117

RESULT 9
CALCANFA
ID CALCANFA STANDARD; PRT; 92 AA.
AC P41547;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor (Fragments).
GN CALC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-25, AND SEQUENCE OF 26-92 FROM N.A.
RX MEDLINE=921100867; PubMed=1758974;
RA Mel J.A., Kwant M.M., Arnold I.C.J., Hazewinkel H.A.W.;
RT "Elucidation of the sequence of canine (pro)-calcitonin. A molecular
RL Regul. Pept. 35:189-195(1991).
CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED BY C-CELLS OF THE THYROID GLAND.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56994; CAA40311.1; ALT_SEQ.
DR HSP; P01262; 1BKU.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.

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KW Hormone; Amidation; Cleavage on pair of basic residues.
FT NON_CONS 25 26
FT PEPTIDE 47 78 CALCITONIN.
FT DISULFID 47 53 BY SIMILARITY.
FT MOD_RES 78 78 AMIDATION (G-79 PROVIDE AMIDE GROUP)
FT NON_TER 92 92 (BY SIMILARITY).
SQ SEQUENCE 92 AA; 9974 MW; 53B103230864039D CRC64;

Query Match 49.2%; Score 90; DB 1; Length 92;
Best Local Similarity 51.5%; Pred. No. 3.8e-06;
Matches 17; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
   I I I I I I I I I I I I I I I I I I
DB 47 CSNLSTCVLGTSKDLNFFHFGSIGFGAETPG 79

RESULT 10
CAL_SHEEP
ID CAL_SHEEP STANDARD; PRT; 143 AA.
AC P01261;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor.
GN CT.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=93246256; PubMed=8482543;
RA Kumaraswamy A., Borges M., Tamir H., Nelkin B.D.;
RT "Cloning of a cDNA encoding sheep calcitonin from a thyroid C-cell
RT library."
RL Gene 126:269-273(1993).
RN [2]
RP SEQUENCE OF 87-118.
RA Sauer R., Niall H.D., Potts J.T. Jr.;
RT "Accelerated procedures for automated peptide degradation."
RL Fed. Proc. 29:728-728(1970).
CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----
DR EMBL; M98053; -; NOT_ANNOTATED_CDS.
DR PIR; JN0580; TCSH.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Amidation; Hormone; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 84
FT PEPTIDE 87 118 CALCITONIN.
FT PROPEP 122 143
FT DISULFID 87 93
FT MOD_RES 118 118 AMIDATION (G-119 PROVIDE AMIDE GROUP).

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SQ SEQUENCE 143 AA; 15658 MW; D4CEB15C5C06B663 CRC64;  
Query Match 39.3%; Score 72; DB 1; Length 143;  
Best Local Similarity 45.5%; Pred. No. 0.0024;  
Matches 15; Conservative 3; Mismatches 15; Indels 0; Gaps 0;  
QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34  
||||| :|: | | | |  
DB 87 CSNLSTCVLSAYWKLDLNNYHRYSGMGFGPTEG 119  
RESULT 11  
KPPR\_SPIOL STANDARD; PRT; 402 AA.  
AC P09559;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)  
DE (Phosphopentokinase) (PRKASE) (PRK).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
[1]  
SEQUENCE FROM N.A.  
RP MEDLINE=88303351; PubMed=2841650;  
RA Roessler K.R., Ogren W.L.;  
RT "Nucleotide sequence of spinach cDNA encoding phosphoribulokinase.";  
RL Nucleic Acids Res. 16:7192-7192(1988).  
[2]  
RP SEQUENCE OF 7-402 FROM N.A.  
RX MEDLINE=88329728; PubMed=2843430;  
RA Milanez S., Mural R.J.;  
RT "Cloning and sequencing of cDNA encoding the mature form of  
RT phosphoribulokinase from spinach.";  
RL Gene 66:55-63(1988).  
[3]  
RP SEQUENCE OF 52-69.  
RX MEDLINE=86129440; PubMed=3004354;  
RA Porter M.A., Milanez S., Stringer C.D., Hartman F.C.;  
RT "Purification and characterization of ribulose-5-phosphate kinase  
RT from spinach.";  
RL Arch. Biochem. Biophys. 245:14-23(1986).  
[4]  
RP SEQUENCE OF 52-69.  
RA Porter M.A., Hartman F.C.;  
RT "Commonality of catalytic and regulatory sites of spinach  
RT phosphoribulokinase: characterization of a tryptic peptide that  
RT contains an essential cysteinyl residue.";  
RL Biochemistry 25:7314-7318(1986).  
[5]  
RN DISULFIDE BOND, AND PARTIAL SEQUENCE.  
RX MEDLINE=88087076; PubMed=2826432;  
RA Porter M.A., Stringer C.D., Hartman F.C.;  
RT "Characterization of the regulatory thioredoxin site of  
RT phosphoribulokinase.";  
RL J. Biol. Chem. 263:123-129(1988).  
CC -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-  
CC ribulose 1,5-bisphosphate.  
CC -!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE  
CC OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.  
CC -!- PATHWAY: Calvin cycle.  
CC -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.  
CC  
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CC EMBL; X07654; CAA30499.1; -  
DR EMBL; M21338; AAB34036.1; ALT\_INIT.  
DR PIR; A25182; A25182.  
DR PIR; A25250; A25250.  
DR PIR; JA0064; JA0064.  
DR PIR; S02099; S02099.  
DR InterPro; IPR001324; PRK.  
DR Pfam; PF00485; PRK; 1.  
DR PRINTS; PR00478; PHRIBLKINASE.  
DR PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.  
KW Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;  
KW ATP-binding; Photosynthesis.  
FT TRANSIT 1 51 CHLOROPLAST.  
FT CHAIN 52 402 PHOSPHORIBULOKINASE.  
FT DISULFID 67 106  
SQ SEQUENCE 402 AA; 45007 MW; 450759B96A675C6B CRC64;  
Query Match 37.2%; Score 68; DB 1; Length 402;  
Best Local Similarity 44.8%; Pred. No. 0.028;  
Matches 13; Conservative 8; Mismatches 8; Indels 0; Gaps 0;  
QY 3 SNLSTCVLGKLSQELHKLQTYPRNTGSG 31  
||||| :|: | | | |  
DB 343 SNLSTKEYGEVTQOMLRHQNFGSNNCTG 371

RESULT 12  
KPPR\_MESCR STANDARD; PRT; 397 AA.  
ID KPPR\_MESCR AC P27774;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)  
DE (Phosphopentokinase) (PRKASE) (PRK).  
OS Mesembryanthemum crystallinum (Common ice plant).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.  
OX NCBI\_TaxID=3544;  
[1]  
RN SEQUENCE FROM N.A.  
RP Michalowski C.B., Derocher E.J., Bohnert H.J., Salvucci M.E.;  
RA Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.  
RL -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-  
CC ribulose 1,5-bisphosphate.  
CC -!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE  
CC OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.  
CC -!- PATHWAY: Calvin cycle.  
CC -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.  
CC  
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CC  
CC EMBL; M73707; AAA3034.1; -  
DR InterPro; IPR001324; PRK.  
DR Pfam; PF00485; PRK; 1.  
DR PRINTS; PR00478; PHRIBLKINASE.  
DR PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.  
KW Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;  
KW ATP-binding; Photosynthesis.  
FT TRANSIT 1 44  
FT CHAIN 45 397 PHOSPHORIBULOKINASE.  
FT DISULFID 62 101 BY SIMILARITY.  
SQ SEQUENCE 397 AA; 44114 MW; 88DC418E211EC975 CRC64;  
Query Match 36.6%; Score 67; DB 1; Length 397;

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Best Local Similarity 44.8%; Pred. No. 0.039;
Matches 13; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 3 SNLSTCVLGLKSQELHKLQTYPRNTGSG 31
||||| : : : : : : : : : :
DB 338 SNLSTKFGYEVTOMLKHQDFPGSNGTG 366

RESULT 13
CAL_BOVIN
ID CAL_BOVIN STANDARD; PRT; 32 AA.
AC P01260;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcitonin.
GN CALC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=70025647; PubMed=5259773;
RA Brewer H.B. Jr., Ronan R.;
RT "Amino acid sequence of bovine thyrocalcitonin.";
RL Proc. Natl. Acad. Sci. U.S.A. 63:940-947(1969).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
DR PIR: A01528; TCBO.
DR InterPro: IPR001693; Calcitonin-like.
DR InterPro: IPR001935; Calcitonin_A.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00270; CALCITONIN.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
DR Hormone; Amidation.
KW DISULFID 1
FT MOD_RES 32 32
SQ SEQUENCE 32 AA; 3596 MW; EDEA2A3ADFFE4909 CRC64;

Query Match 33.9%; Score 62; DB 1; Length 32;
Best Local Similarity 40.6%; Pred. No. 0.013;
Matches 13; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGLKSQELHKLQTYPRNTGSGTP 33
||||| : : : : :
DB 1 CSNLSTCVLSAYWKDLNLYHRFSGMGFGPETP 32

RESULT 14
CAL_PIG
ID CAL_PIG STANDARD; PRT; 32 AA.
AC P01259;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcitonin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=68270618; PubMed=5240032;
RA Potts J.T. Jr., Niall H.D., Keutmann H.T., Brewer H.B. Jr.,
RA Defetos L.J.;
RT "The amino acid sequence of porcine thyrocalcitonin.";
RL Proc. Natl. Acad. Sci. U.S.A. 59:1321-1328(1968).
RN [2]
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RP SEQUENCE.
RX MEDLINE=70161016; PubMed=5462122;
RA Barg W.F. Jr., Englert M.E., Davies M.C., Colucci D.F., Snedeker E.H.,
RA Dziobkowski C., Bell P.H.;
RT "Degradation and structure of porcine calcitonin-1.";
RL Biochemistry 9:1671-1676(1970).
RN [3]
RP SEQUENCE.
RX MEDLINE=69012693; PubMed=5693288;
RA Neher R., Riniker B., Zuber H., Rittel W., Kahnt F.W.;
RT "Thyrocalcitonin. II. Structure of alpha-thyrocalcitonin.";
RL Helv. Chim. Acta 51:917-924(1968).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
DR PIR: A01527; TCGP.
DR InterPro: IPR001693; Calcitonin-like.
DR InterPro: IPR001935; Calcitonin_A.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00270; CALCITONIN.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
DR Hormone; Amidation.
KW DISULFID 1
FT MOD_RES 32 32
SQ SEQUENCE 32 AA; 3607 MW; EDE755ED2FE6EA09 CRC64;

Query Match 33.3%; Score 61; DB 1; Length 32;
Best Local Similarity 40.6%; Pred. No. 0.018;
Matches 13; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGLKSQELHKLQTYPRNTGSGTP 33
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DB 1 CSNLSTCVLSAYWRNLNHFSGMGFGPETP 32

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ID KPPR_ARATH STANDARD; PRT; 395 AA.
AC P25697;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
DE (Phosphopentokinase) (PRKASE) (PRK).
GN AT1G32060 OR t12021.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. C24;
RX MEDLINE=91329732; PubMed=1651130;
RA Horsnell P.R., Raines C.A.;
RT "Nucleotide sequence of a cDNA clone encoding chloroplast
RT phosphoribulokinase from Arabidopsis thaliana.";
RL Plant Mol. Biol. 17:183-184(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
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RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -|- CATALYTIC ACTIVITY: ATP + D-ribose 5-phosphate = ADP + D-
CC ribulose 1,5-bisphosphate.
CC -|- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE
CC OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
CC -|- PATHWAY: Calvin cycle.
CC -|- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X58149; CAA41155.1; -.
DR EMBL; AC074309; AAG50797.1; -.
DR PIR; S16583; S16583.
DR SWISS-2DPAGE; P25697; ARATH.
DR InterPro; IPR001324; PRK.
DR Pfam; PF00485; PRK; 1.
DR PRINTS; PR00478; PHRIBLKINASE.
DR PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.
KW Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
KW ATP-binding; Photosynthesis.
FT TRANSIT 1 46 CHLOROPLAST.
FT CHAIN 47 395 PHOSPHORIBULOKINASE.
FT DISULFID 61 100 BY SIMILARITY.
SQ SEQUENCE 395 AA; 44463 MW; 4660A92EF7E39BC6 CRC64;

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Query Match 33.3%; Score 61; DB 1; Length 395;

Best Local Similarity 41.4%; Pred. No. 0.29;

Matches 12; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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Db 337 SNLSTKFGYEVTTQMKHADFPGSNNGTG 365

Search completed: May 30, 2003, 09:50:56

Job time : 24 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:51:24 ; Search time 18 Seconds  
(without alignments)  
191.200 Million cell updates/sec

Title: SEQ1  
Perfect score: 183  
Sequence: 1 mcsnlstcvlgklsqelhkltqyprntgsgtpg 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	172	94.0	32	10	US-09-847-712-15
2	172	94.0	32	10	US-09-847-712-16
3	172	94.0	32	10	US-09-847-712-17
4	172	94.0	32	10	US-09-847-712-18
5	162	88.5	32	9	US-09-852-870A-20
6	159	86.9	32	10	US-09-847-712-10
7	158	86.3	32	9	US-09-852-870A-21
8	152	83.1	34	9	US-10-131-543-17
9	151	82.5	32	10	US-09-847-712-12
10	149	81.4	32	9	US-09-852-870A-17
11	148	80.9	35	9	US-10-131-543-26
12	147.5	80.6	34	9	US-10-131-543-25
13	147	80.3	35	9	US-10-131-543-24
14	145	79.2	32	9	US-09-852-870A-16
15	144	78.7	31	9	US-10-131-543-12
16	137	74.9	35	9	US-10-131-543-20
17	137	74.9	35	9	US-10-131-543-23
18	136.5	74.6	34	9	US-10-131-543-19
19	136.5	74.6	34	9	US-10-131-543-22

20	136.5	74.6	34	9	US-10-131-543-27
21	136	74.3	35	9	US-10-131-543-18
22	136	74.3	35	9	US-10-131-543-21
23	131	71.6	25	8	US-08-851-965-28
24	123.5	67.5	34	9	US-10-131-543-28
25	118	64.5	25	10	US-09-813-345-20
26	108	59.0	24	10	US-09-813-345-21
27	102	55.7	32	10	US-09-847-712-13
28	101	55.2	116	10	US-09-742-373-7
29	101	55.2	116	10	US-09-742-373-8
30	101	55.2	128	10	US-09-742-373-9
31	101	55.2	141	9	US-09-736-457-1822
32	101	55.2	141	9	US-09-902-941-1822
33	101	55.2	141	9	US-09-849-626-1822
34	101	55.2	141	9	US-10-017-754-1822
35	95	51.9	32	10	US-09-847-712-9
36	95	51.9	32	10	US-09-847-712-19
37	95	51.9	32	10	US-09-847-712-21
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40	89	48.6	32	9	US-09-852-870A-19
41	85	46.4	32	9	US-09-852-870A-18
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44	56	30.6	32	10	US-09-847-712-11
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## ALIGNMENTS

RESULT 1  
US-09-847-712-15  
; Sequence 15, Application US/09847712  
; Patent No. US20020090646A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: REYNOLDS, ANGELA  
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES  
; FILE REFERENCE: A-684  
; CURRENT APPLICATION NUMBER: US/09/847,712  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,511  
; PRIOR FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred embodiments - salmon CT  
; NAME/KEY: misc.feature  
; LOCATION: (32)..(32)  
; OTHER INFORMATION: An Fc domain attached at the C-terminus  
US-09-847-712-15  
Query Match 94.0%; Score 172; DB 10; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.2e-17;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 CSNLTCTVGLKLSQELHKLQYPRNTGSGTP 32  
RESULT 2  
US-09-847-712-16  
; Sequence 16, Application US/09847712  
; Patent No. US20020090646A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, CHUAN-FA

```
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - salmon CT
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus
US-09-847-712-16

Query Match          94.0%; Score 172; DB 10; Length 32;
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 3
US-09-847-712-17
; Sequence 17, Application US/09847712
; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - salmon CT
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: Position 32 is linked to an identical peptide sequence through an
; OTHER INFORMATION: optional linker
US-09-847-712-17
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Query Match          94.0%; Score 172; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 32
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RESULT 4
US-09-847-712-18
; Sequence 18, Application US/09847712
; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
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; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - salmon CT
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the C-terminus
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: Position 32 is linked to an identical peptide sequence through
; OTHER INFORMATION: optional linker
US-09-847-712-18
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Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 20, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osabay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and third Ser
US-09-852-870A-20
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QY 2 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 32
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RESULT 6
US-09-847-712-10
; Sequence 10, Application US/09847712
; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: MARSHALL, WILLIAM S.
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Query Match	Best Local Similarity	Score	DB 10;	Length 32;	Indels	Gaps
Query	2	CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33				
Db	1	CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32				
<p>Query Match 86.9%; Score 159; DB 10; Length 32;            Best Local Similarity 90.6%; Pred. No. 2.1e-15;            Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;</p>						
<p>US-09-852-870A-21</p> <p>Sequence 21, Application US/09852870A</p> <p>Patent No. US20020165132A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Goodman, Murray</p> <p>APPLICANT: Osapay, George</p> <p>TITLE OF INVENTION: Lanthionin Bridged Proteins</p> <p>FILE REFERENCE: LKR 9122-D</p> <p>CURRENT APPLICATION NUMBER: US/09/852,870A</p> <p>CURRENT FILING DATE: 2001-05-10</p> <p>PRIOR APPLICATION NUMBER: US 09/384,601</p> <p>PRIOR FILING DATE: 1999-08-26</p> <p>NUMBER OF SEQ ID NOS: 24</p> <p>SOFTWARE: PatentIn version 3.0</p> <p>SEQ ID NO 21</p> <p>LENGTH: 32</p> <p>TYPE: PRT</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Cys-Ser Lanthionine bridge between Cys and second Ser</p> <p>US-09-852-870A-21</p>						
Query Match	86.3%;	Score 158;	DB 9;	Length 32;		
Best Local Similarity	93.8%;	Pred. No. 2.9e-15;				
Matches	30;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
Query	2	CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33				
Db	1	CGNLSTSVLGKLSQELHKLQTYPRNTGSGTP 32				
<p>Query Match 86.3%; Score 158; DB 9; Length 32;            Best Local Similarity 93.8%; Pred. No. 2.9e-15;            Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>						
<p>US-10-131-543-17</p> <p>Sequence 17, Application US/10131543</p> <p>Publication No. US20030072709A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Pearson, Daniel A.</p> <p>TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS</p> <p>TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS</p> <p>FILE REFERENCE: 09744-016001</p> <p>CURRENT APPLICATION NUMBER: US/10/131,543</p> <p>CURRENT FILING DATE: 2002-04-24</p> <p>PRIOR APPLICATION NUMBER: US 09/694,992</p> <p>PRIOR FILING DATE: 2000-10-24</p> <p>PRIOR APPLICATION NUMBER: PCT/US01/50423</p> <p>PRIOR FILING DATE: 2001-10-24</p> <p>NUMBER OF SEQ ID NOS: 29</p>						



Matches 30; Conservative 1; Mismatches 0; Indels 4; Gaps 1;  
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 Db 1 SNLSTCVLGKLSGGGCKELHKLQTYPRNTGSGTP 35

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 ; Patent No. US20020165132A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodman, Murray  
 ; APPLICANT: Osapay, George  
 ; TITLE OF INVENTION: Lanthionin Bridged Proteins  
 ; FILE REFERENCE: LKR 9122-D  
 ; CURRENT APPLICATION NUMBER: US/09/852,870A  
 ; CURRENT FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: US 09/384,601  
 ; PRIOR FILING DATE: 1999-08-26  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 16  
 ; LENGTH: 32  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and second Ser  
 US-09-852-870A-16

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 Db 1 CGNLSTSVLGKLSQELHKLQTYPRNTDVGATP 32

RESULT 15  
 US-10-131-543-12  
 ; Sequence 12, Application US/10131543  
 ; Publication No. US20030072709A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pearson, Daniel A.  
 ; APPLICANT: Cyr, John E.  
 ; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS  
 ; FILE REFERENCE: 09744-016001  
 ; CURRENT APPLICATION NUMBER: US/10/131,543  
 ; CURRENT FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 09/694,992  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: PCT/US01/50423  
 ; PRIOR FILING DATE: 2001-10-24  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12  
 ; LENGTH: 31  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic construct  
 ; FEATURE:  
 ; NAME/KEY: ACETYLATION  
 ; LOCATION: 1  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 6  
 ; OTHER INFORMATION: Xaa = Hhc: Homohomocysteine  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 13

; OTHER INFORMATION: BAT: N6,N9-bis (mercapto-2-methylpropyl)-6,9-diazanonoic aci  
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 ; NAME/KEY: AMIDATION  
 ; LOCATION: 31  
 US-10-131-543-12

Query Match 78.7%; Score 144; DB 9; Length 31;  
 Best Local Similarity 93.5%; Pred. No. 2.5e-13;  
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 SNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33  
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 Db 1 SNLSTXVLGKLSQELHKLQTYPRNTGSGTP 31

Search completed: May 30, 2003, 09:56:42  
 Job time : 19 secs





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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:41 ; Search time 35 Seconds  
(without alignments)  
129.443 Million cell updates/sec

Title: SEQ1  
Perfect score: 183  
Sequence: 1mcsnlstcvlgklsqelghklqtyprrtntgsqtpg 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database :

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2:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
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10:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
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17:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	183	100.0	34	7 AAP60792	Fish calcitonin de
2	183	100.0	34	9 AAP80414	Salmon calcitonin
3	183	100.0	34	9 AAP80676	Salmon calcitonin-
4	183	100.0	34	9 AAP81041	Sequence of salmon
5	183	100.0	53	22 AAB61575	Partial protein se
6	178	97.3	33	20 ABB08914	Synthetic Cr pepti
7	178	97.3	136	23 ABBG0636	Salmon calcitonin.
8	177	96.7	33	13 AAR30341	[Met 0]-salmon cal
9	174	95.1	33	13 AAR30338	[Leu 0]-salmon cal
10	174	95.1	33	13 AAR30314	[Met 0, Leu 8]-sal

11	173	94.5	33	13	AAR30339	[Val 0]-salmon cal
12	173	94.5	33	13	AAR30340	[Ile 0]-salmon cal
13	172	94.0	32	13	AAP20308	Peptide prepd. by
14	172	94.0	32	5	AAP20389	Sequence of D-Arg
15	172	94.0	32	8	AAP401260	1,7-di-S-acetamid
16	172	94.0	32	8	AAP71487	Sequence of N'alph
17	172	94.0	32	14	AAR363987	Amlylin antagonist
18	172	94.0	32	15	AAR476664	Salmon calcitonin.
19	172	94.0	32	15	AAR476664	Fragment 6 of Sal
20	172	94.0	32	15	AAR59790	Fragment 7 of Sal
21	172	94.0	32	15	AAR60152	Salmon calcitonin
22	172	94.0	32	16	AAR686858	Calcitonin deriv.
23	172	94.0	32	16	AAR84250	Calcitonin peptide
24	172	94.0	32	17	AAR10575	Salmon calcitonin
25	172	94.0	32	18	AAR22342	Salmon agonist pep
26	172	94.0	32	20	AAR704000	Salmon calcitonin
27	172	94.0	32	20	AAR93528	Salmon calcitonin
28	172	94.0	32	20	AAR73387	Salmon calcitonin.
29	172	94.0	32	21	AAV95663	Salmon calcitonin.
30	172	94.0	32	22	AAR91046	Calcitonins (CT) a
31	172	94.0	32	23	AAE14323	Salmon calcitonin
32	172	94.0	32	23	AAE14324	Salmon calcitonin
33	172	94.0	33	13	AAR30342	[Thr 0]-salmon cal
34	172	94.0	33	13	AAR30343	[Ser 0]-salmon cal
35	172	94.0	33	13	AAR30344	[Ala 0]-salmon cal
36	172	94.0	33	13	AAR30345	[Nva 0]-salmon cal
37	172	94.0	33	13	AAR30346	[Nle 0]-salmon cal
38	172	94.0	35	13	AAR20042	Calcitonin analoge
39	172	94.0	64	23	AAE14325	Salmon calcitonin
40	172	94.0	64	23	AAE14326	Salmon calcitonin
41	172	94.0	271	23	AAE14335	Fe-calcitonin fusi
42	172	94.0	33	13	AAR30311	[Val 0,8]-salmon c
43	170	92.9	33	13	AAR30312	[Leu 0, Leu 8]-sal
44	170	92.9	33	13	AAR30313	[file 0, Leu 8]-sal
45	169	92.3	32	7	AAP60858	Salmon 8-Methionin

## ALIGNMENTS

RESULT 1	
AAPE60792	
ID	AAPE60792 standard; Protein; 34 AA.
XX	
XX	AAPE60792;
XX	
XX	17-JUL-1991 (first entry)
XX	
XX	Fish calcitonin derivative.
XX	
XX	pSCTL; E.coli RR1.
XX	
XX	Synthetic.
XX	
Key	Location/Qualifiers
FF	2..34
FT	/label= Peptide of claim 8
FT	27
FT	/label= May be Asn or Asp
FT	28
FT	/label= May be Thr or Val
FT	30
FT	/label= May be Ser or Ala
XX	
XX	<u>W08601226-A.</u>
XX	
PD	<u>27-FEB-1986.</u>
XX	
XX	16-AUG-1985; 85WO-JP00459.
XX	
PR	18-JUN-1985; 85JP-0130815.
PR	17-AUG-1984; 84JP-0170492.
PR	11-MAY-1985; 85JP-0098891.

PR 28-MAY-1985; 85JP-0113254.  
 XX (SAGA ) SAGAMI CHEM RES CENTRE.  
 PA (CENG ) CENTRAL GLASS KK.  
 PA (HODO ) HODOGAYA CHEMICAL KK.  
 PA (NIPS ) NIPPON SODA KK.  
 PA (NISC ) NISSAN CHEMICAL INDS LTD.  
 PA (TOVJ ) TOYO SODA MFG KK.  
 XX Omori M, Miki T, Narushima H, Ikari T, Saito A, Ikushima N;  
 PI Matsumoto R, Watanabe K.  
 XX WPI; 1986-068975/10.  
 DR N-PSDB; AAN60710.  
 XX Biologically active fish calcitonin contg. extra glycine at  
 PT C-terminal - convertible to natural form and prep'd. using E.coli  
 PT recombinant transform.  
 XX Disclosure; Fig 1; 106pp; Japanese.  
 XX The sequence encodes a fish calcitonin derivative which may be used  
 CC for the construction of expression vector pSCT1 capable of  
 CC transforming an E.coli host for the efficient large scale expression  
 CC of the product.  
 XX Sequence 34 AA;  
 SQ Query Match 100.0%; Score 183; DB 7; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 DB 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 RESULT 2  
 AAP80414  
 ID AAP80414 standard; protein; 34 AA.  
 XX  
 AC AAP80414;  
 XX  
 DT 29-OCT-1990 (first entry)  
 XX  
 DE Salmon calcitonin produced by recombinant methods.  
 XX  
 KW Calcitonin; beta-galactosidase; interferon; proinsulin; secretin; inter-  
 KW leukin-2; hirudin; growth hormone releasing factor.  
 XX  
 OS synthetic.  
 XX  
 PN EP286956-A.  
 XX  
 PD 19-OCT-1988.  
 XX  
 PF 06-APR-1988; 88EP-0105438.  
 XX  
 PR 19-FEB-1988; 88DE-3805150.  
 PR 19-FEB-1988; 88DE-3712361.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Wetekam W, Jansen HW, Becker W;  
 XX  
 DR WPI; 1988-294356/42.  
 DR N-PSDB; AAN80970.  
 XX  
 PT Recombinant polypeptide prodn. - via fusion protein with modified beta-  
 PT galactosidase  
 XX  
 PS Example; Page 11; 20pp; German.  
 XX

CC This salmon calcitonin protein is produced as a fusion protein. The  
 CC process can also be used to produce e.g. interferon and proinsulin.  
 XX Sequence 34 AA;  
 SQ Query Match 100.0%; Score 183; DB 9; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 DB 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 RESULT 3  
 AAP80676  
 ID AAP80676 standard; protein; 34 AA.  
 XX  
 AC AAP80676;  
 XX  
 DT 24-OCT-1990 (first entry)  
 XX  
 DE Salmon calcitonin-Gly 33.  
 XX  
 KW 3' terminal hairpin loop; double stranded DNA synthesis;  
 KW salmon calcitonin-Gly 33.  
 XX  
 OS synthetic.  
 XX  
 PN EP292802-A.  
 XX  
 PD 30-NOV-1988.  
 XX  
 PF 13-MAY-1988; 88EP-0107660.  
 XX  
 PR 23-MAY-1987; 87DE-2717436.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Uhlmann E, Hein F;  
 XX  
 DR WPI; 1988-339391/48.  
 DR N-PSDB; N81269  
 XX  
 PT Double stranded DNA prodn -  
 PT from single strand with terminal hairpin loop by filling in  
 PT second strand, then opening or removing hair pin  
 XX  
 PS Disclosure; ; pp; German.  
 XX  
 CC DNA(ds) encoding salmon calcitonin was synthesised as a single  
 CC coding strand with a terminal hairpin primer. The complementary  
 CC strand was synthesised from the primer.  
 CC Use of oligonucleotides with a hairpin loop primer avoids the need  
 CC for chemically synthesising both strands. Also the filling in step  
 CC can be performed using labelled nucleotides to give products  
 CC suitable for use as probes. Mutagenic primers can be used to  
 CC introduce site specific mutations.  
 CC See also AAN81267 and AAN81268.  
 XX  
 SQ Sequence 34 AA;  
 XX  
 CC Query Match 100.0%; Score 183; DB 9; Length 34;  
 CC Best Local Similarity 100.0%; Pred. No. 5.4e-17;  
 CC Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 DB 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 RESULT 4  
 AAP81041

Fri Mayard; protein; 34 AA.

ID  
XX  
XX

AC 03-DEC-1990 (first entry)

DE Sequence of salmon calcitonin I having an additional C-terminal glycine.

XX Hypocalcaemic; hypophosphataemia peptide hormone; pancreatitis therapy.

XX Salmon.

XX EP261552-A.

XX 30-MAR-1988.

XX 15-SEP-1987; 87EP-0113445.

XX 20-SEP-1986; 86DE-3632037.

XX (FARH) HOECHST AG.

XX Hein F, Jansen HW, Muller H, Uhlmann E;

XX WPI; 1988-085860/13.

XX N-PSDB; AAN81385.

XX Salmon calcitonin I derivs. prepn. by inserting new plasmid encoding for the deriv. into e.g. Escherichia coli gene

XX Disclosure; ; p: German.

XX Calcitonin is a hypocalcaemic and hypophosphataemia peptide hormone which regulates serum levels of Ca. It is useful for treating Ca metabolic disorders, as an analgesic and for treating acute pancreatitis inhibiting enzyme secretion.

XX Sequence 34 AA;

Query Match 100.0%; Score 183; DB 9; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34

Db 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34

RESULT 5

ID AAB61575

XX AAB61575 standard; protein; 53 AA.

XX AAB61575;

XX 03-APR-2001 (first entry)

XX Partial protein sequence of pCLYSM.

XX Transgenic; milk; lysozyme; pCLYSM; salmon; calcitonin.

XX Unidentified.

XX WO200100855-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB02459.

XX 23-JUN-1999; 99GB-0014733.

XX 10-AUG-1999; 99US-0147819.

XX (PPLT-) PPL THERAPEUTICS SCOTLAND LTD.

XX Cottingham IR, McCreath GE;

XX WPI; 2001-137958/14.

XX N-PSDB; AAF28653.

XX Producing peptides for use as medicaments, nutritional additives or research tools, comprises expressing a fusion protein, which contains the peptide linked to a lysozyme fusion partner protein, in the milk of a transgenic mammal

XX Example 1; Fig 1; 57pp; English.

XX The present invention relates to a method for producing a peptide. The method comprises expressing in the milk of a transgenic non-human placental mammal a fusion protein, comprising the peptide to be expressed linked to lysozyme (a fusion partner protein). The method is useful for producing proteins or peptides that are useful as medicaments, nutritional additives or research tools. The present sequence is a partial DNA sequence of pCLYSM. pCLYSM was designed to express a human lysozyme-salmon calcitonin fusion protein in the milk of transgenic animals. The fusion protein allows the release of calcitonin from the end of a linker arm fused to the lysozyme C terminal by cyanogen bromide chemical cleavage. pCLYSM consists of the ovine beta-lactoglobulin (BLG) promoter and 5' UTR, human lysozyme gene, peptide linker (see AAB61572), CNBr cleavage site and flanking region, chick alpha-globin UTR, polyadenylation site and the pUC18 bacterial plasmid vector. The present sequence is a partial protein sequence of pCLYSM comprising the peptide linker, the CNBr cleavage site and the calcitonin peptide sequence.

XX Sequence 53 AA;

Query Match 100.0%; Score 183; DB 22; Length 53;

Best Local Similarity 100.0%; Pred. No. 8.7e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34

Db 20 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 53

RESULT 6

ID ABB08914

XX ABB08914 standard; peptide; 33 AA.

XX AC ABB08914;

XX 16-JUL-2002 (first entry)

XX Synthetic CT peptide sCT(Gly).

XX TNF; tumour necrosis factor; beta-sheet; fusion protein; recombinant production; Escherichia coli; TNF fusion vector; PT7-T150; PT7-T57; CT; sCT; PT150-sCT(Gly).

XX Synthetic.

XX KRL33475-B1.

XX 21-APR-1998.

XX 04-APR-1994; 94KR-0007018.

XX 04-APR-1994; 94KR-0007018.

XX (HANL-) HANIL SYNTHETIC FIBER CO LTD.

XX Shin H, Jang S, Kim D, kang S;

XX WPI; 1999-617508/53.

CC ligand that confers transcellular, transcytotic or paracellular  
 CC transporting properties to an agent specifically bound to the ligand,  
 CC where (II) is not an antibody. Alternatively, (I) comprises two or more  
 CC (II) directed to one or more ligands. (I) is useful for delivering a  
 CC biologically active agent to an animal, for transporting an active agent  
 CC through an epithelial or mucosal barrier, and for treating or  
 CC identifying a disease in an animal e.g. diseases of the respiratory  
 CC system including lung cancer and tumours, asthma, pathogenic infections,  
 CC allergy-related disorders, gastrointestinal tract disorders, disorders  
 CC relating to gastrointestinal hormones, Chron's disease, eating disorders  
 CC and any disease or disorder involving polyclonal immunoglobulin receptor (pIgR)  
 CC displaying cells. This is the amino acid sequence of a protein associated  
 CC with the transport of biologically active agents across cellular  
 CC barriers.  
 XX  
 SQ Sequence 136 AA:

Query Match 97.3% Score 178; DB 23; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 1.le-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 34  
 |||||||  
 Db 83 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 115

RESULT 8  
 AAR30341  
 ID AAR30341 standard; peptide: 33 AA.

XX AC AAR30341:  
 XX AC  
 DT 30-APR-1993 (first entry)  
 DE [Met O]-salmon calcitonin.  
 KW sCT; calcium regulation; thyroid gland; hormone; bone resorption.  
 XX Salmon.  
 OS  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /note= "Designated position 0, i.e. additional  
 FT N-terminal amino acid "  
 FT Disulfide-bond 2..8  
 FT Modified-site 33  
 FT /note= "amidated"  
 FT  
 PN WO9221369-A.  
 PD 10-DEC-1992.  
 PP 03-JUN-1992; 92WO-US04854.  
 PP 05-JUN-1991; 91US-0711180.  
 XX (VICA-) VICAL INC.  
 PA  
 XX Basava C, Hostetler KY;  
 PI WPI; 1992-433374/52.  
 DR  
 XX New synthetic calcitonin peptide(as) are hypocalcaemic agents -  
 PT for treating Paget's disease, osteoporosis, bone fracture, etc.  
 PT with lower immunogenicity than natural calcitonin(s)  
 XX  
 PS Example 17c: Page 29; 42pp; English.  
 XX  
 CC This hypocalcaemic peptide is an example of novel  
 CC calcitonin analogues which have amino acid additions at the  
 CC N-terminal which, alone or with other substitutions, and with  
 CC deletions at other residues, act to improve potency, prolong  
 CC duration of the hormonal effect and increase oral or nasal  
 CC CC

CC associated with these diseases or with articular rheumatism. The  
CC peptides also inhibit gastrin secretion making them useful to  
CC treat acute pancreatitis and gastrointestinal disorders, esp.  
CC gastric ulcers.  
XX  
SQ Sequence 33 AA; 95.1%; Score 174; DB 13; Length 33;  
Query Match Best Local Similarity 97.0%; Pred. No. 8e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0;

QY 1 ACSNLSTCVLGRKSSQELHKLQTYPRNTGSGTP 33  
Db 1 LCSNLSTCVLGRKSSQELHKLQTYPRNTGSGTP 33

RESULT 10  
AAR30314  
ID AAR30314 standard; peptide; 33 AA.

XX  
DT 30-APR-1993 (first entry)  
XX

XX  
KW  
XX

	Key	Location/Qualifiers
XX		
FH		
FT	Misc-difference 1	

FT	Disulfide-bond	2..8
FT	Misc-difference	9

FT		/note= "designated position 8 in scf,"
FT		Leu replaces Val"
FT	Modified-site	33
FT		/note= "amidated"

XX  
PN WO9221369-A.  
XX  
PD 10-DEC-1992.

XX	03-JUN-1992;	92WO-US04854.
PF		
XX		
DP	05-TUN-1001.	Q1HS-0711180

XX  
PA (VICA-) VICAL INC.  
XX  
XX  
BT Baccara C. Hoetzel, KY.

XX  
DR  
XX  
WPI; 1992-433374/52.  
XX

PT for treating Paget's disease, osteoporosis, bone fracture, etc.  
PT with lower immunogenicity than natural calcitonin(s)  
XX

XX This hypocalcaemic peptide is an example of novel  
CC  
CC calcitonin analogues which have amino acid additions at the

CC deletions at other residues, act to improve potency, prolong  
CC duration of the hormonal effect and increase oral or nasal  
CC bioavailability, c.f. native CTS. The analogues can be used to

metabolism. They are thus useful for treating e.g. Vitamin D intoxication, hyperparathyroidism, idiopathic hypercalcaemia of infancy, bone fracture, rickets, osteoporosis and bone pain

CC peptides also inhibit gastrin secretion making them useful to

CC treat acute pancreatitis and gastrointestinal disorders, esp.  
 CC gastric ulcers.  
 XX Sequence 33 AA;  
 50

Query Match 95.1%; Score 174; DB 13; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 8e-16; Indels 0; Gaps 0;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCSNLSTCVLGLKLSQELHKLQTPRTNTGSGTP 33  
 Db 1 MCSNLSTCVLGLKLSQELHKLQTPRTNTGSGTP 33

RESULT 11  
 AAR30339  
 ID AAR30339 standard; peptide: 33 AA.  
 XX  
 AC AAR30339;  
 XX  
 DT 30-APR-1993 (first entry)  
 XX  
 DE [Ile O]-salmon calcitonin.  
 XX  
 KW SCT; calcium regulation; thyroid gland; hormone; bone resorption.  
 XX  
 OS Salmon.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "designated position 0, i.e. additional  
 FT Disulfide-bond 2..8 N-terminal amino acid"  
 FT Modified-site 33 /note= "amidated"  
 FT  
 PN W09221369-A.  
 XX  
 PD 10-DEC-1992.  
 XX  
 PF 03-JUN-1992; 92WO-US04854.  
 XX  
 PR 05-JUN-1991; 91US-0711180.  
 XX  
 PA (VICA-) VICAL INC.  
 XX  
 PI Basava C, Hostetler KY;  
 XX  
 WPI; 1992-433374/52.  
 XX  
 CC New synthetic calcitonin peptide(as) are hypocalcaemic agents -  
 CC for treating Paget's disease, osteoporosis, bone fracture, etc.  
 CC with lower immunogenicity than natural calcitonin(s)  
 CC  
 PS Example 17a; Page 29; 42pp; English.  
 CC  
 CC This hypocalcaemic peptide is an example of novel  
 CC calcitonin analogues which have amino acid additions at the  
 CC N-terminal which, alone or with other substitutions, and with  
 CC deletions at other residues, act to improve potency, prolong  
 CC duration of the hormonal effect and increase oral or nasal  
 CC bioavailability. c.f. native CTs. The analogues can be used to  
 CC reduce or normalise serum calcium levels or to influence bone  
 CC metabolism. They are thus useful for treating e.g. Vitamin D  
 CC deficiency, hyperparathyroidism, idiopathic hypercalcaemia of  
 CC malignancy, fracture rickets, osteoporosis and bone pain  
 CC associated with these diseases or with articular rheumatism. The  
 CC peptides also inhibit gastrin secretion making them useful to  
 CC treat acute pancreatitis and gastrointestinal disorders, esp.

Query Match 94.5%; Score 173; DB 13; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 1.1e-15;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCSNLSTCVLGLKLSQELHKLQTPRTNTGSGTP 33  
 Db 1 VCSNLSTCVLGLKLSQELHKLQTPRTNTGSGTP 33

RESULT 12  
 AAR30340  
 ID AAR30340 standard; peptide: 33 AA.  
 XX  
 AC AAR30340;  
 XX  
 DT 30-APR-1993 (first entry)  
 XX  
 DE [Ile O]-salmon calcitonin.  
 XX  
 KW SCT; calcium regulation; thyroid gland; hormone; bone resorption.  
 XX  
 OS Salmon.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "designated position 0, i.e. additional  
 FT Disulfide-bond 2..8 N-terminal amino acid"  
 FT Modified-site 33 /note= "amidated"  
 FT  
 PN W09221369-A.  
 XX  
 PD 10-DEC-1992.  
 XX  
 PF 03-JUN-1992; 92WO-US04854.  
 XX  
 PR 05-JUN-1991; 91US-0711180.  
 XX  
 PA (VICA-) VICAL INC.  
 XX  
 PI Basava C, Hostetler KY;  
 XX  
 WPI; 1992-433374/52.  
 XX  
 CC New synthetic calcitonin peptide(as) are hypocalcaemic agents -  
 CC for treating Paget's disease, osteoporosis, bone fracture, etc.  
 CC with lower immunogenicity than natural calcitonin(s)  
 CC  
 PS Example 17b; Page 29; 42pp; English.  
 CC  
 CC This hypocalcaemic peptide is an example of novel  
 CC calcitonin analogues which have amino acid additions at the  
 CC N-terminal which, alone or with other substitutions, and with  
 CC deletions at other residues, act to improve potency, prolong  
 CC duration of the hormonal effect and increase oral or nasal  
 CC bioavailability. c.f. native CTs. The analogues can be used to  
 CC reduce or normalise serum calcium levels or to influence bone  
 CC metabolism. They are thus useful for treating e.g. Vitamin D  
 CC deficiency, hyperparathyroidism, idiopathic hypercalcaemia of  
 CC malignancy, fracture rickets, osteoporosis and bone pain  
 CC associated with these diseases or with articular rheumatism. The  
 CC peptides also inhibit gastrin secretion making them useful to  
 CC treat acute pancreatitis and gastrointestinal disorders, esp.  
 CC  
 SQ Sequence 33 AA;

Query Match 94.5%; Score 173; DB 13; Length 33;  
 Best Local Similarity 97.0%; Pred. No. 1.1e-15;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCSNLSTCVLGLKLSQELHKLQTPRTNTGSGTP 33

14-JAN-1992 (first entry)

PI Flanigan E;  
XX  
DR WPI: 1987-129186/18.  
XX  
PT New salmon and eel calcitonin analogues - do not have disulphide  
XX bond connecting cysteine residues.  
PS  
XX Claim 1: page 9-10; 10pp: English.  
XX  
CC The salmon calcitonin analogue has the biological activity of the same  
CC type of calcitonin and comparable potency to known calcitonins.  
CC It differs in not having a disulphide bond connecting the cysteines at  
CC positions 1 and 7. In a test, 3 and 9 MU/100 g body weight of the  
CC standard salmon calcitonin and 0.2 ml/100 g body weight of the  
CC analogue were given to different rats. Serum calcium was determined  
CC after 1 hr. The standard salmon calcitonin was found to contain  
CC 4000 IU/mg, whereas the analogue assayed at 4250 IU/mg.  
XX  
SQ Sequence 32 AA:  
Query Match 94.0%; Score 172; DB 8; Length 32;  
Best Local Similarity 100.0%; Pos 8 No  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 CSNLSCTVLGKLSQELHKLOTYPRTNTGSGTP 33  
DB 1 CSNLSCTVLGKLSQELHKLOTYPRTNTGSGTP 32

Search completed: May 30, 2003, 09:50:26  
Job time : 37 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: May 30, 2003, 09:49:44 : Search time 15 Seconds  
(without alignments)  
217.905 Million cell updates/sec  
Title: SEQ1  
Perfect score: 183  
Sequence: 1 mcsnlstcvlgklsqelhkltqyprntgsgtpg 34  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR-73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	178	97.3	56	2 I51029	calcitonin 1 - pink salmon (fragment)
2	178	97.3	59	2 I51260	calcitonin 1 - pink salmon (fragment)
3	178	97.3	136	1 TCON	calcitonin 1 - pink salmon (fragment)
4	159	86.9	32	1 TCON2	calcitonin 1 - pink salmon (fragment)
5	157	85.8	32	1 TCON2C	calcitonin 1 - pink salmon (fragment)
6	157	85.8	32	1 TCON2P	calcitonin 1 - pink salmon (fragment)
7	157	85.8	32	1 TCON3	calcitonin 1 - pink salmon (fragment)
8	157	85.8	138	1 TCON3	calcitonin 1 - pink salmon (fragment)
9	154	84.2	32	1 TCON3	calcitonin 1 - pink salmon (fragment)
10	108	59.0	136	1 TCON3	calcitonin 1 - pink salmon (fragment)
11	101	55.2	141	1 TCON3	calcitonin 1 - pink salmon (fragment)
12	101	55.2	141	2 A41716	calcitonin 1 - pink salmon (fragment)
13	100	54.6	136	2 JC4977	calcitonin 1 - pink salmon (fragment)
14	96	52.5	137	2 A35934	calcitonin 1 - pink salmon (fragment)
15	90	49.2	67	2 A60063	calcitonin 1 - pink salmon (fragment)
16	72	39.3	143	1 TCON3	calcitonin 1 - pink salmon (fragment)
17	68	37.2	402	2 S02099	calcitonin 1 - pink salmon (fragment)
18	67	36.6	397	2 T12436	calcitonin 1 - pink salmon (fragment)
19	62	33.9	32	1 TCON3	calcitonin 1 - pink salmon (fragment)
20	61	33.3	32	1 TCON3	calcitonin 1 - pink salmon (fragment)
21	61	33.3	395	2 S16583	calcitonin 1 - pink salmon (fragment)
22	61	33.3	404	2 S16585	calcitonin 1 - pink salmon (fragment)
23	61	33.3	404	2 S16585	calcitonin 1 - pink salmon (fragment)
24	58	31.7	438	2 S62453	calcitonin 1 - pink salmon (fragment)
25	57	31.1	334	2 A02321	calcitonin 1 - pink salmon (fragment)
26	57	31.1	352	2 T06463	calcitonin 1 - pink salmon (fragment)
27	55	30.1	664	2 AG1026	calcitonin 1 - pink salmon (fragment)
28	54.5	29.8	213	2 B23750	calcitonin 1 - pink salmon (fragment)
29	54.5	29.8	401	2 A69713	calcitonin 1 - pink salmon (fragment)

30	54	29.5	489	2	A81166	type II site-speci
31	52.5	28.7	727	2	H69724	DNA topoisomerase
32	52	28.4	375	2	T08167	phosphoribulokinas
33	51	27.9	491	2	S47217	alpha-2-antiplasmi
34	51	27.9	685	2	B82606	conjugal transfer
35	50.5	27.6	431	2	T27904	hypothetical prote
36	50.5	27.6	435	2	T46443	hypothetical prote
37	49	26.8	619	2	A82638	DNA topoisomerase
38	49	26.8	939	2	S38653	ecae protein (enter
39	49	26.8	952	2	S38653	transposase - Kieb
40	48.5	26.5	352	2	H71836	hypothetical prote
41	48	26.2	159	2	G70841	hypothetical prote
42	48	26.2	180	2	S70725	rec15 protein - fi
43	48	26.2	224	2	A84948	NADH2 dehydrogenas
44	48	26.2	309	2	AD1130	B. subtilis transc
45	48	26.2	355	2	G82247	cysteine synthase/

ALIGNMENTS

RESULT 1

I51029

calcitonin 1 - pink salmon (fragment)

C:Species: Oncorhynchus gorbuscha (pink salmon)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C:Accession: I51029; S42985

R:Marital, K.; Maubras, L.; Taboulet, J.; Jullienne, A.; Berry, M.; Milhaud, G.; Bens

Proc. Natl. Acad. Sci. U.S.A. 91, 4912-4914, 1994

A:Title: The calcitonin gene is expressed in salmon gills.

A:Reference number: I51029; MUID:94255438; PMID:8197156

A:Accession: I51029

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-56 <MAR>

A:Cross-references: EMBL:X78080; NID:g459540; PIDN:CAA54988.1; PID:g459541

A:Gene: calc I

C:Superfamily: calcitonin

F:1-56/Product: procalcitonin 1 (fragment) #status predicted <MAT1>

F:3-34/Product: calcitonin 1 #status predicted <MAT2>

Query Match 97.3%; Score 178; DB 2; Length 56;

Best Local Similarity 100.0%; Pctd No. 8.4e-18;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSCTVLGKLSQELHKLTQYPRNTGSGTGP 34

Db 3 CSNLSCTVLGKLSQELHKLTQYPRNTGSGTGP 35

RESULT 2

I51260

calcitonin 1 - pink salmon (fragment)

C:Species: Oncorhynchus gorbuscha (pink salmon)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I51260; T51260

R:Marital, K.; Maubras, L.; Taboulet, J.; Jullienne, A.; Milhaud, G.; Moukhtar, M.S.;

Gen 149, 277-281, 1994

A:Title: Production of salmon calcitonin I in Oncorhynchus gorbuscha by alternative p

A:Reference number: I51260; MUID:95047488; PMID:7959002

A:Accession: I51260

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-59 <MA2>

A:Cross-references: GB:S74352; NID:g786497; PIDN:AAD14151.1; PID:g4261851

A:Accession: I51261

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-59 <MA2>

A:Cross-references: GB:S74353; NID:g786498

C:Genetics: CT

## C.Superfamily: calcitonin

Query Match 97.3%; Score 178; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 8.8e-18;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 34  
|||||  
Db 6 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 38

## RESULT 3

## TCOIN

calcitonin 1 precursor - salmon  
C:Species: Oncorhynchus sp. (salmon)  
C:Date: 24-Apr-1984 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C:Accession: A31229; A93772; A01530  
R:Poesschl, E.; Lindley, I.; Hofer, E.; Seifert, J.M.; Brunowsky, W.; Besemer, J.  
FEBS Lett. 226, 96-100, 1987  
A:Title: The structure of prolactin of the salmon as deduced from its cDNA sequence.  
A:Reference number: A31229; MUID:88083644; PMID:3691820  
A:Accession: A31229  
A:Molecule type: mRNA  
A:Residues: 1-136 <NDA>  
A:Cross-references: GB:Y00765; NID:G64312; PID:G64313  
A:Note: The species of the source is not indicated but is designated as Oncorhynchus ket  
R:Niall, H.D.; Keutmann, H.T.; Copp, D.H.; Potts Jr., J.T.  
Proc. Natl. Acad. Sci. U.S.A. 64, 771-778, 1969  
A:Title: Amino acid sequence of salmon ultimobranchial calcitonin.  
A:Reference number: A93772; MUID:70053602; PMID:5361048  
A:Accession: A93772  
A:Molecule type: protein  
A:Residues: 83-114 <NTA>  
R:Gutmann, S.; Pless, J.; Huguenin, R.L.; Sandrin, E.; Bossert, H.; Zehnder, K.  
Helv. Chim. Acta 52, 1789-1795, 1969  
A:Title: Synthese von Salm-calcitonin, einem hochaktiven hypocalcaemischen Hormon.  
A:Reference number: A91631; MUID:70067983; PMID:5361911  
A:Contents: annotation; synthesis of hormone  
C:Superfamily: calcitonin  
A:Note: The proposed structure of the natural hormone was supported by that of the synth  
C:Keywords: amidated carboxyl end; hormone  
F:1-25/Domains: signal sequence #status predicted <SIG>  
F:26-136/Product: prolactin 1 #status predicted <PCA>  
F:83-114/Product: calcitonin 1 #status experimental <CAI>  
F:83-89/Disulfide bonds: #status experimental  
F:114/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 97.3%; Score 178; DB 1; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 34  
|||||  
Db 83 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 115

## RESULT 4

## TCOIN

calcitonin - Japanese eel  
C:Species: Anguilla japonica (Japanese eel)  
C:Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 08-Dec-1995  
C:Accession: A01529  
R:Noda, T.; Narita, K.  
J. Biochem. 79, 353-359, 1976  
A:Title: Amino acid sequence of eel calcitonin.  
A:Reference number: A01529  
A:Accession: A01529  
A:Molecule type: protein  
A:Residues: 1-32 <NOD>  
C:Superfamily: calcitonin  
C:Keywords: amidated carboxyl end  
F:1-7/Disulfide bonds: #status experimental  
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 86.9%; Score 159; DB 1; Length 32;  
Best Local Similarity 90.6%; Pred. No. 2.2e-15;  
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 33  
|||||  
Db 1 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 32

## RESULT 5

## TCOIN

calcitonin 2 - sockeye salmon  
C:Species: Oncorhynchus nerka (sockeye salmon)  
C:Date: 22-May-1981 #sequence\_revision 22-May-1981 #text\_change 23-Aug-1996  
C:Accession: A01531  
R:Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr.,  
in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S.,  
A:Title: Chemistry and physiology of the calcitonins: some recent advances.  
A:Reference number: A04616  
A:Accession: A01531  
A:Molecule type: protein  
A:Residues: 1-32 <KEU>  
R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttmann, S.  
Nature New Biol. 240, 62-63, 1972  
A:Title: Synthesis of two natural salmon calcitonins.  
A:Reference number: A93406; MUID:73047885; PMID:4508400  
A:Contents: annotation; synthesis  
A:Note: the synthetic hormones were the same as the natural ones on the basis of phys  
an calcitonins 1 or 2  
C:Superfamily: calcitonin  
C:Keywords: amidated carboxyl end; hormone  
F:1-7/Disulfide bonds: #status experimental  
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 85.8%; Score 157; DB 1; Length 32;  
Best Local Similarity 87.5%; Pred. No. 4.1e-15;  
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSQELHKLQTYPRNTGSGTPG 33  
|||||  
Db 1 CSNLSVCVLGKLSQELHKLQTYPRNTGAGVP 32

## RESULT 6

## TCOIN

calcitonin 2 - chum salmon  
C:Species: Oncorhynchus keta (chum salmon)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Aug-1996  
C:Accession: C01531; A01531  
R:Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr.,  
in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S.,  
A:Title: Chemistry and physiology of the calcitonins: some recent advances.  
A:Reference number: A04616  
A:Accession: C01531  
A:Molecule type: protein  
A:Residues: 1-32 <KEU>  
R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttmann, S.  
Nature New Biol. 240, 62-63, 1972  
A:Title: Synthesis of two natural salmon calcitonins.  
A:Reference number: A93406; MUID:73047885; PMID:4508400  
A:Contents: annotation; synthesis  
A:Note: the synthetic hormones were the same as the natural ones on the basis of phys  
an calcitonins 1 or 2  
C:Superfamily: calcitonin  
C:Keywords: amidated carboxyl end; hormone  
F:1-7/Disulfide bonds: #status experimental  
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 85.8%; Score 157; DB 1; Length 32;  
Best Local Similarity 87.5%; Pred. No. 4.1e-15;  
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
    |||||
Db 1 CSNLSTCVLGKLSQDLHKLQTFPRNTGAGVP 32

RESULT 7
TCOIN2P
C:Species: Oncorhynchus gorbuscha (pink salmon)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Aug-1996
C:Accession: D01531; A01531
R:Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr., J.T.
in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S., ed.
A:Title: Chemistry and physiology of the calcitonins: some recent advances.
A:Reference number: A04616
A:Accession: D01531
A:Molecule type: protein
A:Residues: 1-32 <KEU>
R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttman, S.
Nature New Biol. 240, 62-63, 1972
A:Title: Synthesis of two natural salmon calcitonins.
A:Reference number: A93406; MUID:73047885; PMID:4508400
A:Contents: annotation; synthesis
A>Note: the synthetic hormones were the same as the natural ones on the basis of physica
an calcitonins 1 or 2
C:Superfamily: calcitonin
C:Keywords: amidated carboxyl end; hormone
F:1-7/Disulfide bonds: #status experimental
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 85.8%; Score 157; DB 1; Length 32;
Best Local Similarity 87.5%; Pred. No. 4.1e-15;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
    |||||
Db 1 CSNLSTCVLGKLSQDLHKLQTFPRNTGAGVP 32

RESULT 8
TCCH
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C:Accession: S00153; A25725; A24415; I50182; A22467
R:Minvielle, S.; Cressent, M.; Delehay, M.C.; Segond, N.; Milhaud, G.; Jullienne, A.; M
FEBS Lett. 223, 63-68, 1987
A:Title: Sequence and expression of the chicken calcitonin gene.
A:Reference number: S00153; MUID:88030046; PMID:3666142
A:Accession: S00153
A:Molecule type: DNA
A:Residues: 1-138 <MIN>
A:Cross-references: EMBL:X06311
A>Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; the
R:Lasmoles, F.; Jullienne, A.; Day, F.; Minvielle, S.; Milhaud, G.; Moukhtar, M.S.
EMBO J. 4, 2603-2607, 1985
A:Title: Elucidation of the nucleotide sequence of chicken calcitonin mRNA: direct evide
A:Reference number: A25725; MUID:86030240; PMID:4054101
A:Accession: A25725
A:Molecule type: mRNA
A:Residues: 12-55, 'E', 57-138 <LAS>
A:Cross-references: EMBL:X03012; NID:g63157; PIDN:CAA26796.1; PID:g63158
R:Honna, T.; Watanabe, M.; Hirose, S.; Kanai, A.; Kangawa, K.; Matsuo, H.
J. Biochem. 100, 459-467, 1986
A:Title: Isolation and determination of the amino acid sequence of chicken calcitonin I
A:Reference number: A24415; MUID:87057104; PMID:3782060
A:Accession: A24415
A:Molecule type: protein
A:Residues: 1-32 <HOM>
R:Lasmoles, F.; Jullienne, A.; Desplan, C.; Milhaud, G.; Moukhtar, M.S.
FEBS Lett. 180, 113-116, 1985
A:Title: Structure of chicken calcitonin predicted by partial nucleotide sequence of its

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A:Reference number: I50182; MUID:85102042; PMID:3838160
A:Accession: I50182
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 71-117 <LA2>
A:Cross-references: GB:M27563; NID:g211373; PIDN:AAA48648.1; PID:g211374
C:Comment: The calcitonin gene codes for two mRNA species by tissue-specific alternat
ripheral nervous system codes for calcitonin gene-related peptide.
C:Genetics:
A:Introns: 29/2; 73/2
C:Superfamily: calcitonin
C:Keywords: alternative splicing; amidated carboxyl end; hormone
F:82-113/Product: calcitonin #status experimental <MAT>
F:82-88/Disulfide bonds: #status experimental
F:113/Modified site: amidated carboxyl end (Pro) (amide in mature form from following
Query Match 85.8%; Score 157; DB 1; Length 138;
Best Local Similarity 84.8%; Pred. No. 1.7e-14;
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 34
    |||||
Db 82 CASLSTCVLGKLSQELHKLQTYPRTDVGATPG 114

RESULT 9
TCOIN3
calcitonin 3 - coho salmon
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 08-Dec-1995
C:Accession: B01531; A01531
R:Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr.,
in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S.,
A:Title: Chemistry and physiology of the calcitonins: some recent advances.
A:Reference number: A04616
A:Accession: B01531
A:Molecule type: protein
A:Residues: 1-32 <KEU>
R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttman, S.
Nature New Biol. 240, 62-63, 1972
A:Title: Synthesis of two natural salmon calcitonins.
A:Reference number: A93406; MUID:73047885; PMID:4508400
A:Contents: annotation; synthesis
A>Note: the synthetic hormones were the same as the natural ones on the basis of phys
an calcitonins 1 or 2
C:Superfamily: calcitonin
C:Keywords: amidated carboxyl end
F:1-7/Disulfide bonds: #status experimental
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 84.2%; Score 154; DB 1; Length 32;
Best Local Similarity 84.4%; Pred. No. 1.1e-14;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
    |||||
Db 1 CSNLSTCVLGKLSQDLHKLQTFPRNTGAGVP 32

RESULT 10
TCRT
calcitonin precursor - rat
N:Contains: amino-terminal procalcitonin cleavage peptide (N-proCT); carboxyl-termina
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 18-Jun-1999
C:Accession: A94259; A93853; A91236; I52379; A01525
R:Jacobs, J.W.; Goodman, R.H.; Chin, W.W.; Bee, P.C.; Habener, J.F.; Bell, N.H.; Pott
Science 213, 457-459, 1981
A:Title: Calcitonin messenger RNA encodes multiple polypeptides in a single precursor
A:Reference number: A94259; MUID:81225842; PMID:6264603
A:Accession: A94259
A:Molecule type: mRNA
A:Residues: 1-136 <JAC>

```



Query Match 49.2%; Score 90; DB 2; Length 67;  
Best Local Similarity 51.5%; Pred. No. 1.9e-05;  
Matches 17; Conservative 5; Mismatches 11; Indels 0; Gaps 0;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:44 ; Search time 79 Seconds  
(without alignments)  
88,679 Million cell updates/sec

Title: SEQ1

Perfect score: 183

Sequence: 1 mesnlstcvgklsgelkhlqtpyrtngstgtpg 34

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

1: sp.archaea.\*

2: sp.bacteria.\*

3: sp.fungi.\*

4: sp.human.\*

5: sp.invertebrate.\*

6: sp.mammal.\*

7: sp.mhc.\*

8: sp.organelle.\*

9: sp.phage.\*

10: sp.plant.\*

11: sp.rodent.\*

12: sp.virus.\*

13: sp.vertibrate.\*

14: sp.unclassified.\*

15: sp.rvirus.\*

16: sp.bacteriap.\*

17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	97.3	56	Q91157	Q91157 oncorhynch
2	178	97.3	59	Q91970	Q91970 oncorhynch
3	178	97.3	62	Q92163	Q92163 oncorhynch
4	172	94.0	32	Q8Q684	Q8Q684 oncorhynch
5	172	94.0	32	Q8Q682	Q8Q682 oncorhynch
6	172	94.0	32	Q8Q673	Q8Q673 oncorhynch
7	172	94.0	32	Q8Q672	Q8Q672 salmo salar
8	172	94.0	32	Q8Q671	Q8Q671 oncorhynch
9	172	94.0	32	Q8Q670	Q8Q670 salvelinus
10	169	92.3	32	Q8Q683	Q8Q683 oncorhynch
11	166	90.7	136	Q8Q678	Q8Q678 fugu rubrip
12	159	86.9	32	Q9PS21	Q9PS21 carassius a
13	158	86.3	62	Q79813	Q79813 oncorhynch
14	157	85.8	65	Q9W623	Q9W623 gallus gall
15	156	85.2	50	Q9QYCA	Q9QYCA paralichthy
16	112	61.2	140	Q9NOV5	Q9NOV5 equus caball

17	101	55.2	93	4	Q13935	Q13935 homo sapien
18	96	52.5	48	11	Q88610	Q88610 mus musculus
19	90	49.2	130	6	Q9MYV2	Q9MYV2 canis famill
20	58	31.7	396	10	Q95033	Q95033 odontella s
21	57	31.1	334	16	Q8YPR9	Q8YPR9 anabaena sp
22	57	31.1	352	10	P93681	P93681 pisum sativ
23	56	30.6	405	10	Q9ATC3	Q9ATC3 vaucheria l
24	55	30.1	664	16	Q9RHF5	Q9RHF5 salmonella
25	54	29.5	473	2	Q9XAZ6	Q9XAZ6 neisseria m
26	54	29.5	489	16	Q9K091	Q9K091 neisseria m
27	53.5	29.2	103	6	Q9BGW1	Q9BGW1 macaca fasc
28	53	29.0	233	15	Q8Q805	Q8Q805 human immun
29	53	29.0	279	16	Q9CNF6	Q9CNF6 pasteurella
30	52.5	28.7	310	11	Q9D9D4	Q9D9D4 mus musculus
31	52.5	28.7	327	16	P96583	P96583 bacillus su
32	52	28.4	321	13	Q98871	Q98871 brachydanio
33	52	28.4	462	11	Q35255	Q35255 mus musculus
34	52	28.4	462	11	Q99L30	Q99L30 mus musculus
35	51	27.9	164	4	Q96EV5	Q96EV5 homo sapien
36	51	27.9	685	16	Q9PBT0	Q9PBT0 xylella fas
37	51	27.9	1066	2	Q8RNQ8	Q8RNQ8 legionella
38	51	27.9	1332	5	Q8SZZ7	Q8SZZ7 drosophila
39	51	27.9	1472	5	Q9V358	Q9V358 drosophila
40	50.5	27.6	152	5	Q9NIF9	Q9NIF9 metacnephia
41	50.5	27.6	435	4	Q9NTA2	Q9NTA2 homo sapien
42	50.5	27.6	439	5	Q23526	Q23526 caenorhabdi
43	50.5	27.6	687	2	Q937B7	Q937B7 pseudomonas
44	50.5	27.6	687	2	Q8RSH4	Q8RSH4 uncultured
45	50	27.3	83	10	Q8S8P8	Q8S8P8 arabidopsis

## ALIGNMENTS

### RESULT 1

ID	Q91157	PRELIMINARY;	PRT;	56 AA.
AC	Q91157;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Calcitonin (Fragment).			
GN	CALC I.			
OS	Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8017;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=GILL;			
RX	MEDLINE=94255438; PubMed=8197156;			
RA	Martial K., Maubras L., Taboulet J., Jullienne A., Berry M.,			
RA	Milhaud G., Benson A.A., Moukhtar M.S., Cressent M.;			
RT	"The calcitonin gene is expressed in salmon gills.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4912-4914(1994).			
DR	EMBL; X78080; CAA54988.1;			
DR	HSSP; P01262; I8K0.			
DR	InterPro; IPR001693; Calcitonin-like.			
DR	InterPro; IPR001935; Calcitonin_A.			
DR	Pfam; PF00214; Calc_CGRP_IAPP; 1.			
DR	PRINTS; PR00270; CALCITONIN.			
DR	SMART; SM00113; CALCITONIN; 1.			
DR	PROSITE; PS00258; CALCITONIN; 1.			
FT	NON_TER	1	34	CALCITONIN.
FT	CHAIN	3	34	B073F85C56C1848F CRC64;
SQ	SEQUENCE	56 AA;	6165 MW;	

Query Match 97.3%; Score 178; DB 13; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.9e-20;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSCTVGLKLSQELHKLQTPYRTNNGSGTGP 34

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DR PRINTS: PRO0270; CALCITONIN_A.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
FT NON_TER 1
SQ SEQUENCE 62 AA; 6865 MW; EE8AA50D5ED4CA99 CRC64;

Query Match 97.3%; Score 178; DB 13; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
   |||||||
Db 9 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 41

RESULT 4
Q8QG84 PRELIMINARY; PRT; 32 AA.
ID Q8QG84
AC Q8QG84;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8017;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three
RT Different Sources.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF491872; AAL99993.1; -.
FT NON_TER 1 32
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match 94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
   |||||||
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 5
Q8QG82 PRELIMINARY; PRT; 32 AA.
ID Q8QG82
AC Q8QG82;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN Oncorhynchus sp. FY-02.
OS Oncorhynchus sp. FY-02.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=190488;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three
RT Different Sources.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF491874; AAL99995.1; -.
FT NON_TER 1 32
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;
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Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 6
Q8QG73 ID Q8QG73 PRELIMINARY; PRT; 32 AA.
AC Q8QG73;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus sp. BZ-2002.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=192133;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497755; AAM18086.1; -.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 7
Q8QG72 ID Q8QG72 PRELIMINARY; PRT; 32 AA.
AC Q8QG72;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497756; AAM18087.1; -.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 8
Q8QG71 ID Q8QG71 PRELIMINARY; PRT; 32 AA.
AC Q8QG71;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus kisutch (Coho salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8019;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497757; AAM18088.1; -.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 9
Q8QG70 ID Q8QG70 PRELIMINARY; PRT; 32 AA.
AC Q8QG70;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Salvelinus alpinus (Arctic char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8036;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497758; AAM18089.1; -.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

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RESULT 10
ID Q8QG83 PRELIMINARY; PRT; 32 AA.
AC Q8QG83;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three
RT Different Sources.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491873; AAL99994.1; -.
FT NON_TER 1 1
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3462 MW; AFC935406807E7C2 CRC64;

Query Match 92.3%; Score 169; DB 13; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.9e-19;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSOELHKLQTYPTNTGSGTP 33
Db 1 CSNLSTCVLGKLSOELHKLQTYPTNTGNGTP 32

RESULT 11
ID Q8QFT8 PRELIMINARY; PRT; 136 AA.
AC Q8QFT8;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin.
GN CALC.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark M.S.;
RT "Structure and expression of Fugu calcitonin gene.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309015; CAC81278.1; -.
FT CHAIN 83 114
SQ SEQUENCE 136 AA; 14997 MW; A9A9FA80D3E584E4 CRC64;

Query Match 90.7%; Score 166; DB 13; Length 136;
Best Local Similarity 90.9%; Pred. No. 6.1e-18;
Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSOELHKLQTYPTNTGSGTPG 34
Db 83 CSNLSTCVLGKLSOELHKLQTFPRTNVGAGTPG 115

RESULT 12
ID Q9PS21 PRELIMINARY; PRT; 32 AA.
AC Q9PS21;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

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DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calcitonin, CT.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE.
RX MEDLINE=93202415; PubMed=8454163;
RA Saseyama Y., Ukawa K., Kai-Ya H., Oguro C., Takei Y., Watanabe T.X.,
RA Nakajima K., Sakakibara S.;
RT "Goldfish calcitonin: purification, characterization, and hypocalcemic
RT potency.";
RL Gen. Comp. Endocrinol. 89:189-194 (1993).
DR HSP; P01262; IBKU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
SQ SEQUENCE 32 AA; 3390 MW; AFC93549F818560F CRC64;

Query Match 86.9%; Score 159; DB 13; Length 32;
Best Local Similarity 90.6%; Pred. No. 1.4e-17;
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSOELHKLQTYPTNTGSGTP 33
Db 1 CSSLSTCVLGKLSOELHKLQTYPTNVGAGTP 32

RESULT 13
ID P79813 PRELIMINARY; PRT; 62 AA.
AC P79813;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calcitonin 4 (Fragment).
OS Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8017;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97057244; PubMed=8901583;
RA Jansz H., Martial K., Zandberg J., Milhaud G., Benson A.A.,
RA Julienne A., Moukhtar M.S., Cressent M.;
RT "Identification of a new calcitonin gene in the salmon Oncorhynchus
RT gorbuscha.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12344-12348 (1996).
DR EMBL; U71286; AAB38532.1; -.
DR HSP; P01262; IBKU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
FT NON_TER 1 1
FT CHAIN 1 6
FT CHAIN 9 40
FT CHAIN 45 62
SQ SEQUENCE 62 AA; 6860 MW; 1316EEB8EACF199 CRC64;

Query Match 86.3%; Score 158; DB 13; Length 62;
Best Local Similarity 84.8%; Pred. No. 4.4e-17;
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSOELHKLQTYPTNTGSGTPG 34

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DB 9 CSNLSTCVLGKLSQDLHKLOTFFRTDVGAGTPG 41

RESULT 14

Q9W6Z3	PRELIMINARY;	PRT;	65 AA.
AC	Q9W6Z3;		
ID	Q9W6Z3;		
DT	01-NOV-1999 (TrEMBLrel. 12, Created)		
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)		
DE	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Calcitonin/CGRP gene exon 4.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OC	NCBI_TaxID=9031;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=88030046; PubMed=3666142;		
RA	Minvielle S., Cressent M., Delehaie M.C., Second N., Milhaud G.,		
RA	Jullienne A., Moukhtar M.S., Lasmoules F.;		
RL	"Sequence and expression of the chicken calcitonin.";		
RT	FEBS Lett. 223:63-68(1987).		
DR	EMBL; X06313; CAA29632.1; -.		
DR	HSSP; P01262; 1BKU.		
DR	InterPro; IPR001693; Calcitonin-like.		
DR	InterPro; IPR001935; Calcitonin.A.		
DR	Pfam; PF00214; Calc_CGRP_IAPP; 1.		
DR	PRINTS; PR00270; CALCITONIN.		
DR	SMART; SM00113; CALCITONIN; 1.		
DR	PROSITE; PS00258; CALCITONIN; 1.		
DR	SEQUENCE 65 AA; 7232 MW; 772C54DA8A5ABC0B CRC64;		

RESULT 15

Q90VC4	PRELIMINARY;	PRT;	50 AA.
ID	Q90YC4		
AC	Q90YC4		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-NAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Calcitonin (fragment).		
DE	CT/CGRP.		
OS	Paralichthys olivaceus (flounder).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthopterygii; Acanthopterygii; Percomorpha; Pleuronectiformes;		
OC	Pleuronectoidei; Paralichthyidae; Paralichthys.		
OX	NCBI_TaxID=8255;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21406117; PubMed=11514025;		
RA	Suzuki N., Suzuki T., Kurokawa T.;		
RT	"Cloning of a calcitonin gene-related peptide from genomic DNA and its		
RT	mRNA expression in flounder, Paralichthys olivaceus.";		
RL	Peptides 22:1435-1438(2001).		
RL	EMBL; AB052782; BAB64410.1; -;		
DR	InterPro: IPR001693; Calcitonin-like.		
DR	Pfam: PF00214; Calc_CGRP_IRRP; 1.		
FT	NON_TER 1		
FT	CHAIN 1		
FT	SEQUENCE 50 AA; 5426 MW; ABD8859A27DA249F CRC64;		
SQ			
Query Match		85.2%;	Score 156; DB 13; Length 50;

Best Local Similarity 81.8%; Pred. No. 7.1e-17;  
Matches 27; Conservative 4; Mismatches 2

Search completed: May 30, 2003, 09:53:05  
Job time : 81 secs



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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:44 ; Search time 14 seconds  
(without alignments)  
71.456 Million cell updates/sec

Title: SEQ1

Perfect score: 183

Sequence: 1 mcsnlstcvlgklsqelhkltqyprntngsgtpg 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*  
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5: /cgn2.6/ptodata/1/1aa/PTCUS.COMB.pep.\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	178	97.3	33 1 US-07-776-272-7	Sequence 7, Appli
2	172	94.0	32 1 US-07-952-735A-6	Sequence 6, Appli
3	172	94.0	32 1 US-08-164-408A-6	Sequence 6, Appli
4	172	94.0	32 1 US-08-164-408A-7	Sequence 7, Appli
5	172	94.0	32 1 US-07-794-288D-4	Sequence 4, Appli
6	172	94.0	32 1 US-08-176-153-2	Sequence 2, Appli
7	172	94.0	32 1 US-08-424-866-4	Sequence 4, Appli
8	172	94.0	32 1 US-08-477-727A-6	Sequence 6, Appli
9	172	94.0	32 1 US-08-477-727A-18	Sequence 18, Appli
10	172	94.0	32 1 US-08-477-727A-31	Sequence 31, Appli
11	172	94.0	32 1 US-08-477-727A-43	Sequence 43, Appli
12	172	94.0	32 2 US-08-595-868C-38	Sequence 38, Appli
13	172	94.0	32 3 US-08-847-007A-2	Sequence 2, Appli
14	172	94.0	32 3 US-09-071-090-2	Sequence 2, Appli
15	172	94.0	32 4 US-09-139-819A-38	Sequence 38, Appli
16	172	94.0	32 4 US-09-750-913-38	Sequence 38, Appli
17	172	94.0	32 5 PCT-US93-12692-2	Sequence 2, Appli
18	172	94.0	32 5 PCT-US94-14303-2	Sequence 2, Appli
19	172	94.0	32 5 PCT-US96-05372-4	Sequence 4, Appli
20	172	94.0	32 6 5183802-3	Patent No. 5183802
21	165	90.2	33 1 US-07-776-272-8	Sequence 8, Appli
22	163	89.1	32 3 US-08-907-602-1	Sequence 1, Appli
23	162	88.5	32 3 US-08-467-472C-20	Sequence 20, Appli
24	162	88.5	32 4 US-09-384-061-20	Sequence 20, Appli
25	159	86.9	32 1 US-07-952-735A-5	Sequence 5, Appli
26	159	86.9	32 1 US-08-490-669-3	Sequence 3, Appli
27	159	86.9	32 1 US-08-424-866-1	Sequence 1, Appli

28	159	86.9	32 2 US-08-322-386B-2	Sequence 2, Appli
29	159	86.9	32 2 US-08-595-868C-37	Sequence 37, Appli
30	159	86.9	32 3 US-08-847-007A-3	Sequence 3, Appli
31	159	86.9	32 3 US-09-071-090-3	Sequence 3, Appli
32	159	86.9	32 4 US-09-139-819A-37	Sequence 37, Appli
33	159	86.9	32 4 US-09-750-913-37	Sequence 37, Appli
34	159	86.9	32 5 PCT-US96-05372-1	Sequence 1, Appli
35	159	86.9	32 6 5183802-4	Patent No. 5183802
36	158	86.3	32 3 US-08-467-472C-21	Sequence 21, Appli
37	158	86.3	32 4 US-09-384-061-21	Sequence 21, Appli
38	157	85.8	32 2 US-08-595-868C-39	Sequence 39, Appli
39	157	85.8	32 4 US-09-139-819A-39	Sequence 39, Appli
40	157	85.8	32 4 US-09-750-913-39	Sequence 39, Appli
41	157	85.8	33 1 US-07-776-272-9	Sequence 9, Appli
42	155	84.7	31 3 US-08-847-007A-7	Sequence 7, Appli
43	155	84.7	31 3 US-09-071-090-7	Sequence 7, Appli
44	154	84.2	32 2 US-08-595-868C-40	Sequence 40, Appli
45	154	84.2	32 3 US-07-401-432-45	Sequence 45, Appli

## ALIGNMENTS

### RESULT 1

US-07-776-272-7  
; Sequence 7, Application US/07776272  
; Patent No. 5612454  
; GENERAL INFORMATION:  
; APPLICANT: Kaminuma, Toshihiko  
; APPLICANT: Iida, Toshi  
; APPLICANT: Tajima, Masahiro  
; TITLE OF INVENTION: Process for Purification of Polypeptide  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wegner, Cantor, Mueller & Player  
; STREET: 1233 20th St. N.W. P.O. Box 18218  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: United States of America  
; ZIP: 20036-8218  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07776,272  
; FILING DATE: 19911129  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: P-450-23167  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-0400  
; TELEFAX: 202-887-0605  
; TELEX: 440706  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Salmon  
; US-07-776-272-7

Query Match 97.3%; Score 178; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.4e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSCTCVLGKLSQELHKLQYPRNTNGSGTPG 34

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; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wigman, Cohen, Leitner, & Myers, P.C.
; STREET: 1735 Jefferson Davis Hwy., Suite 200
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, Kb storage
; COMPUTER: IQ 486
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,408A
; FILING DATE: 09-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Herbert
; REGISTRATION NUMBER: 25,109
; REFERENCE/DOCKET NUMBER: 3721-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-4300
; TELEFAX: (703)413-8129
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: Ser at position 2 substituted
; OTHER INFORMATION: Ser with tert-butyl
; OTHER INFORMATION: 5 substituted with tert-butyl
; OTHER INFORMATION: 4 substituted with tert-butyl
; OTHER INFORMATION: Tyr at position 6 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 6 substituted with tert-butyl
; OTHER INFORMATION: Lys at position 11 substituted with tert-butyl
; OTHER INFORMATION: Lys at position 13 substituted with tert-butyl
; OTHER INFORMATION: Glu at position 15 substituted with tert-butyl
; OTHER INFORMATION: His at position 17 substituted with trityl
; OTHER INFORMATION: Lys at position 18 substituted with t-butoxycarbonyl
; OTHER INFORMATION: Thr at position 21 substituted with tert-butyl
; OTHER INFORMATION: Tyr at position 22 substituted with tert-butyl
; OTHER INFORMATION: Arg at position 24 substituted with
; OTHER INFORMATION: 2,2,5,7,8-pentamethylchroman-6-sulphonyl
; OTHER INFORMATION: Thr at position 25 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 27 substituted with tert-butyl
; OTHER INFORMATION: Ser at position 29 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 31 substituted with tert-butyl
US-08-164-408A-6
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Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CSNLSCTCVLKGSLQELHKLQTYPRNTGSGTP 33
DB 1 CSNLSCTCVLKGSLQELHKLQTYPRNTGSGTP 32
RESULT 4
US-08-164-408A-7
; Sequence 7, Application US/08164408A
; Patent No. 5527881
; GENERAL INFORMATION:
; APPLICANT: Poblet, Marcos C
; APPLICANT: Obols, Berta P.
; APPLICANT: Farres, Gemma J.
; TITLE OF INVENTION: Procedure for Preparing Salmon
; TITLE OF INVENTION: Calcitonin
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

```



```

; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 92-20C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 427
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 32
; OTHER INFORMATION: /label= amidated
; OTHER INFORMATION: /note= "C-terminal Proline residue is amidated."
US-08-176-153-2

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 32

RESULT 7
US-08-424-866-4
; Sequence 4, Application US/08424866
; Patent No. 5721207
; GENERAL INFORMATION:
; APPLICANT: NO. 5721207le, John F.
; APPLICANT: Abajian, Henry B.
; TITLE OF INVENTION: Method of Treatment of Pain
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,866
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33878
; REFERENCE/DOCKET NUMBER: 1-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORGANISM: Salmon
; ORIGINAL SOURCE:
US-08-424-866-4

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 32

RESULT 8
US-08-477-727A-6
; Sequence 6, Application US/08477727A
; Patent No. 5739106
; GENERAL INFORMATION:
; APPLICANT: Rink, Timothy
; APPLICANT: Young, Andrew
; APPLICANT: Beeley, Nigel
; APPLICANT: Prickett, Kathryn
; TITLE OF INVENTION: APPETITE REGULATING
; COMPOSITIONS
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 633 WEST FIFTH STREET, SUITE 4700
; CITY: LOS ANGELES
; STATE: CA
; COUNTRY: USA
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,727A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DUFT, BRADFORD J
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 214/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-8400
; TELEFAX: 619-552-0157
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-477-727A-6

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 33
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RESULT 9
US-08-477-727A-18
; Sequence 18, Application US/08477727A
; Patent No. 5739106

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Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 32

RESULT 8
US-08-477-727A-6
; Sequence 6, Application US/08477727A
; Patent No. 5739106
; GENERAL INFORMATION:
; APPLICANT: Rink, Timothy
; APPLICANT: Young, Andrew
; APPLICANT: Beeley, Nigel
; APPLICANT: Prickett, Kathryn
; TITLE OF INVENTION: APPETITE REGULATING
; COMPOSITIONS
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 633 WEST FIFTH STREET, SUITE 4700
; CITY: LOS ANGELES
; STATE: CA
; COUNTRY: USA
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,727A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DUFT, BRADFORD J
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 214/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-8400
; TELEFAX: 619-552-0157
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-477-727A-6

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPRNTGSGTP 33
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RESULT 9
US-08-477-727A-18
; Sequence 18, Application US/08477727A
; Patent No. 5739106

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Fri May 30 10:10:21 2003

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; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-595-868C-38
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Query Match 94.0%; Score 172; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSNLSTCVLKGKLSQELHKLTQYPRNTGSGTP 32

RESULT 13
US-08-847-007A-2
; Sequence 2, Application US/08847007A
; Patent No. 6083480
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Bush, Larry R
; APPLICANT: Pearson, Daniel P
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Radiolabeled Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,007A
; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083480nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..7
; OTHER INFORMATION: /label= Disulfide bond
; OTHER INFORMATION: /notes= A disulfide bond exists between the
; OTHER INFORMATION: two sulfur atoms of the cysteine residues;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 32
; OTHER INFORMATION: /label= Amide
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OTHER INFORMATION: /note= "The carboxyl terminus is modified to an amide"  
 OTHER INFORMATION: amide"  
 US-08-847-007A-2

Query Match 94.0%; Score 172; DB 3; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 CSNLSCTCVLGLKSOELHKLQTYPRNTGSGTP 32

RESULT 14  
 US-09-071-090-2  
 ; Sequence 2, Application US/09071090  
 ; Patent No. 6086850  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dean, Richard T.  
 ; APPLICANT: Bush, Larry R.  
 ; APPLICANT: Pearson, Daniel A.  
 ; APPLICANT: Lister-James, John  
 ; TITLE OF INVENTION: CALCITONIN RECEPTOR BINDING REAGENTS  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Diatide, Inc.  
 ; STREET: 9 Delta Drive  
 ; CITY: Londonderry  
 ; STATE: NH  
 ; COUNTRY: USA  
 ; ZIP: 03053

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,090  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/847,007  
 FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: McDaniel, Patricia A.  
 REGISTRATION NUMBER: 33,194  
 REFERENCE/DOCKET NUMBER: DITI 125.1PCT  
 TELEPHONE: (603) 437-8970  
 TELEFAX: (603) 437-8977

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: both  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: CALCITONIN--SALMON  
 FEATURE:  
 NAME/KEY: Disulfide-bond  
 LOCATION: 1..7  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 32  
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 OTHER INFORMATION: /label= amide  
 US-09-071-090-2

Query Match 94.0%; Score 172; DB 3; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 CSNLSCTCVLGLKSOELHKLQTYPRNTGSGTP 32

RESULT 15  
 US-09-139-819A-38  
 ; Sequence 38, Application US/09139819A  
 ; Patent No. 6251635  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WAGNER, Fred W.  
 ; APPLICANT: STOUT, Jay S.  
 ; APPLICANT: HENRIKSEN, Dennis B.  
 ; APPLICANT: PARTRIDGE, Bruce E.  
 ; APPLICANT: HOLMQUIST, Bart  
 ; APPLICANT: FRANK, Julie A.

TITLE OF INVENTION: RECOMBINANT PREPARATION OF CALCITONIN  
 TITLE OF INVENTION: FRAGMENTS AND USE THEREOF IN THE PREPARATION OF CALCITONIN  
 NUMBER OF SEQUENCES: 51  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY & LARDNER  
 STREET: 3000 K Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20007-5109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/139,819A  
 FILING DATE: 25-AUG-1998  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/595,868  
 FILING DATE: 06-FEB-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 089187/0144  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-139-819A-38

Query Match 94.0%; Score 172; DB 4; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSCTCVLGLKSOELHKLQTYPRNTGSGTP 33  
 Db 1 CSNLSCTCVLGLKSOELHKLQTYPRNTGSGTP 32

Search completed: May 30, 2003, 09:51:38  
 Job time : 15 secs

